



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 168824**

**TO: Celine Qian**  
**Location: rem/2A64/2C70**  
**Art Unit: 1636**  
**Monday, May 15, 2006**  
**Case Serial Number: 09/921143**

**From: Toby Port**  
**Location: Biotech-Chem Library**  
**REM-1A59**  
**Phone: (571)272-2523**

**toby.port@uspto.gov**

### **Search Notes**

Dear Examiner Qian,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Toby Port  
Technical Information Specialist  
STIC Biotech/Chem Library  
(571)272-2523



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# STIC SEARCH RESULTS FEEDBACK FORM

## Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher* or *contact:*

Mary Hale, Information Branch Supervisor  
Remsen Bldg. 01 D86  
571-272-2507

## Voluntary Results Feedback Form

➤ I am an examiner in Workgroup:  Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature  
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC-Biotech-Chem Library Remsen Bldg.



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ACCESS DB # 188 824  
PLEASE PRINT CLEARLY

CRAFT

Scientific and Technical Information Center

SEARCH REQUEST FORM

Requester's Full Name: Celine Qian Examiner # 78710 Date: 5/4/06  
Art Unit: 1636 Phone Number: 2-0777 Serial Number: 09/921,143  
Location (Bldg/Room#): 2A64 (Mailbox #): 2670 Results Format Preferred (circle): PAPER DISK  
\*\*\*\*\*

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following: ME

Title of Invention: Vascular endothelial growth factor-2

Inventors (please provide full names): Coleman, T.

Earliest Priority Date: 8/3/2000

Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search SEQ ID NO:36 (both commercial & interference database).

STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: _____	____ NA Sequence (#)	____ STN      ____ Dialog
Searcher Phone #: _____	____ AA Sequence (#)	____ Questel/Orbit      ____ Lexis/Nexis
Searcher Location: _____	____ Structure (#)	____ Westlaw      ____ WWW/Internet
Date Searcher Picked Up: _____	____ Bibliographic	____ In-house sequence systems
Date Completed: _____	____ Litigation	____ Commercial      ____ Oligomer      ____ Score/Length
Searcher Prep & Review Time: _____	____ Fulltext	____ Interference      ____ SPDI      ____ Encode/Transl
Online Time: _____	____ Other	____ Other (specify)

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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using bw model

Run on: May 13, 2006, 17:29:01 ; Search time 17095 Seconds  
(without alignments)  
17566.771 Million cell updates/sec

Title: US-09-921-143-36

Perfect score: 5283

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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

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1: gb\_ba:\*  
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11: gb\_sy:\*  
12: gb\_un:\*  
13: gb\_vl:\*  
14: gb\_htg:\*  
15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	2312.6	43.8	8786	11	AY622810
3	2309.6	43.7	9816	11	AY622811
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8	2177.4	41.2	2604	11	AY189826
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DEFINITION  
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VERSION  
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Bannasch, D. and Schwab, M.  
A versatile bait vector for rapid Gal4 dependent two-hybrid screens  
Unpublished  
2 (bases 1 to 6074)  
Bannasch, D.  
Direct Submission  
Submitted (30-OCT-1998) D. Bannasch, Institution Division of,  
Cytogenetics/H0400 Deutsches, Krebsforschungszentrum (DKFZ), Im  
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Revised by author 10-JUN-1999  
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Best Local Similarity 94.5%; Pred. No. 0;
Matches 2568; Conservative 0; Mismatches 5; Indels 145; Gaps 1;

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Db 2430 CGGCGCGCCCTGCGCTGACAGCGGAAACCGCGCGCATTAAGCAGCGGATGTCTGTTG 2489
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LOCUS	AY622811 9816 bp DNA circular SYN 14-MAR-2005
DEFINITION	Shuttle reporter vector pSUN119, complete sequence.
ACCESSION	AY622811
VERSION	AY622811.1 GI:60651286
KEYWORDS	
SOURCE	Shuttle reporter vector pSUN119
ORGANISM	Shuttle reporter vector pSUN119
REFERENCE	other sequences; artificial sequences; vectors.
TITLE	1 (bases 1 to 9816)
JOURNAL	Argueta, C., Yukeek, K. and Summers, M.
PUBMED	Construction and use of GFP reporter vectors for analysis of
AUTHORS	cell-type-specific gene expression in Nostoc punctiforme
TITLE	J. Microbiol. Methods 59 (2), 181-188 (2004)
JOURNAL	15369854
FEATURES	2 (bases 1 to 9816)
source	Argueta, C., Yukeek, K. and Summers, M.L.
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	Sc., Northridge, CA 91330-8303, USA
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RESULT 4  
AR260588  
LOCUS AR260588 8349 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 16 from patent US 6489542.  
ACCESSION AR260588  
VERSION AR260588.1 GI:27311143  
KEYWORDS  
SOURCE Unknown.





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LOCUS	SYN8KRCG	2661 bp	DNA linear SYN 27-Apr-1993
DEFINITION	Synthetic plasmid pK18 (pBRNeO/pUC18) Kanamycin resistance gene, complete cds.		
ACCESSION	M17626		
VERSION	M17626.1	GI:207845	
KEYWORDS	complete genome; kanamycin resistance.		
SOURCE	unidentified cloning vector		
ORGANISM	unidentified cloning vector		
REFERENCE	other sequences; artificial sequences; vectors.		
AUTHORS	1 (bases 1 to 2661)		
JOURNAL	Pridmore, R.D.		
PUBMED	New and versatile cloning vectors with kanamycin-resistance marker		
COMMENT	Gene 56 (2-3), 309-312 (1987)		
FEATURES	Original source text: Plasmid pBRNeO and pUC18 DNA.		
source	Location/Qualifiers		
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			Gaps	1
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2383	ACATACGAGCCGGAAGCATTAAGCTGTAAAGCTTGGGTGCTTATGTAGTACCTTA	2324		
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ORIGIN

Query Match 42.0%; Score 2218.4; DB 11; Length 2999;  
Best Local Similarity 93.4%; Pred. No. 0;  
Matches 2388; Conservative 0; Mismatches 26; Indels 144; Gaps 1;

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VERSION ccdB gene; kanamycin resistance.  
KEYWORDS Cloning vector pK1119  
SOURCE Cloning vector pK1119  
ORGANISM Other sequences; artificial sequences; vectors.  
REFERENCE 1 (bases 1 to 2999)  
AUTHORS Bernard, P.  
TITLE New ccdB positive-selection cloning vectors with kanamycin or  
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ORIGIN

Query Match 42.0%; Score 2218.4; DB 11; Length 2999;  
Best Local Similarity 93.4%; Pred. No. 0;  
Matches 2388; Conservative 0; Mismatches 26; Indels 144; Gaps 1;

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 Lee,D.W., Haag,J.R. and Aramayo,R.  
 Construction of strains for rapid homokaryon purification after  
 integration of constructs at the histidine-3 (his-3) locus of  
 Neurospora crassa  
 Curr. Genet. 43 (1), 17-23 (2003)  
 JOURNAL  
 PUBMED 12684841  
 REFERENCE  
 2 (bases 1 to 2604)  
 Lee,D.W., Haag,J.R. and Aramayo,R.  
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his-3 integration vector pJHAM002  
other sequences; artificial sequences; vectors.  
1 (bases 1 to 11373)  
Lee,D.W., Haag,J.R. and Aramayo,R.  
Construction of strains for rapid homokaryon purification after  
integration of constructs at the histidine-3 (his-3) locus of  
Neurospora crassa  
Curr. Genet. 43 (1), 17-23 (2003)  
JOURNAL  
PUBMED 12684841  
REFERENCE 2 (bases 1 to 11373)  
AUTHORS Lee,D.W., Haag,J.R. and Aramayo,R.  
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 TITLE Construction of strains for rapid homokaryon purification after integration of constructs at the histidine-3 (his-3) locus of Neurospora crassa  
 JOURNAL Curr. Genet. 43 (1), 17-23 (2003)  
 PUBMED 12684841  
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 AUTHORS Lee,D.W., Haag,J.R. and Aramayo,R.  
 TITLE Direct Submision  
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 Tools for genetic engineering in the amino acid-producing bacterium  
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 Direct Substitution  
 Submitted (15-JAN-2003) Department of Genetics, University of  
 Bielefeld, Universitaetstrasse 25, Bielefeld D-33615, Germany  
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ORIGIN

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AUTHORS			Kirchner,O. and Tauch,A.
TITLE			Tools for genetic engineering in the amino acid-producing bacterium
JOURNAL			Corynebacterium glutamicum
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TITLE			Kirchner,O. and Tauch,A.
JOURNAL			Submitted (22-JUN-2003) Department of Genetics, University of
REFERENCE			Bielefeld, Universitaetsstrasse 25, Bielefeld D-33615, Germany
FEATURES			Location/Qualifiers
SOURCE			1..5695
			/organism="Shuttle vector pEC-K19mob2"



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VERSION AY219861.1 GI:29164983

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Shuttle vector pEC-K19MECA2  
Shuttle vector pEC-K19MECA2  
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Kirchner,O. and Tauch,A.  
Tools for genetic engineering in the amino acid-producing bacterium  
Corynebacterium glutamicum  
J. Biotechnol. 104 (1-3), 287-299 (2003)

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## ORIGIN

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VERSION AF445080.1 GI:17386067  
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ORGANISM Cloning vector pEC-Kl8mob2  
REFERENCE Cloning sequences; artificial sequences; vectors.  
AUTHORS 1 (bases 1 to 5695)  
Tauch,A., Kirchner,O., Löffler,B., Gotker,S., Puhler,A. and  
Kalinowski,J.  
TITLE Efficient Electroporation of Corynebacterium diptheriae with  
a Mini-Replicon Derived from the Corynebacterium glutamicum Plasmid  
pGAI  
Curr. Microbiol. 45 (5), 362-367 (2002)  
JOURNAL  
PUBMED 12232668  
REFERENCE 2 (bases 1 to 5695)  
AUTHORS Tauch,A.  
JOURNAL Direct Submission  
TITLE Submitted (08-NOV-2001) Department of Genetics, University of  
Bielefeld, Universitätsstrasse 25, Bielefeld D-33615, Germany  
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CC factor 2 (VEGF-2) insert. The nucleic acid is useful for producing a host  
 CC cell by transducing, transforming or transfecting a host cell with the  
 CC DNA and for treating a patient having chronic limb ischaemia or  
 CC myocardial ischaemia, or a disease or disorder selected from autoimmune  
 CC disorders (e.g. rheumatoid arthritis, dermatitis), allergic reactions or  
 CC conditions (e.g. asthma), organ rejection, inflammatory conditions (e.g.  
 CC Crohn's disease), hyperproliferative disorders (e.g. Gaucher's disease),  
 CC diseases due to viral, bacterial, fungal or parasitic infection,  
 CC cardiovascular disorders (e.g. cardiomyopathy), arrhythmia, heart valve  
 CC diseases, aneurysms, arterial occlusive disorders and embolism. This  
 CC sequence represents the pVGI.1 expression vector containing the VEGF-2  
 CC insert

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Db 2281 TAAAGTGAAGAAAGCCTGGGCTAATCAAGGGGTGCTCAAGCTCTCTCTTAACTGGATTGT 2340
QY 2341 CCTATGTCTCTTTGCTTCTGTGCTGTGTATGTCTGTGCTGTGTGATGATGATGATGATG 2400
Db 2341 CCTATGTCTCTTTGCTTCTGTGCTGTGTATGTCTGTGCTGTGTGATGATGATGATGATG 2400
QY 2401 GCAGTGGCAACAATGAGCTGGGTGAGAGCCCGGGGGGAGGGTGAACCTTCAACCTTGGCA 2460
Db 2401 GCAGTGGCAACAATGAGCTGGGTGAGAGCCCGGGGGGAGGGTGAACCTTCAACCTTGGCA 2460
QY 2461 CTGAGAGTGGCCCGGAGAGACCGGGCATCGTGTGATGATGATGATGATGATGATGATGATG 2520
Db 2461 CTGAGAGTGGCCCGGAGAGACCGGGCATCGTGTGATGATGATGATGATGATGATGATGATG 2520
QY 2521 CTCTACCAACTGAGGAACTACTGCAACTAGGCCCACTACCTGTCTGACCCCTCTGCA 2580
Db 2521 CTCTACCAACTGAGGAACTACTGCAACTAGGCCCACTACCTGTCTGACCCCTCTGCA 2580
QY 2581 ATGAATATAAACCTTGAAGAAGCACTCAAGTGTGTGTATCATGCGTGCATGTGCATATG 2640
Db 2581 ATGAATATAAACCTTGAAGAAGCACTCAAGTGTGTGTATCATGCGTGCATGTGCATATG 2640
QY 2641 TGGTGCAGGGGGGAACTAGAGTGGGGCTGCTGAGTGTGCGGGCTTAATCTATCTGCA 2700
Db 2641 TGGTGCAGGGGGGAACTAGAGTGGGGCTGCTGAGTGTGCGGGCTTAATCTATCTGCA 2700
QY 2701 GCTGTCTAGACGTATCATGTGTATAGCTGTTTCTGTGTGAAATGTTATCGCTACA 2760
Db 2701 GCTGTCTAGACGTATCATGTGTATAGCTGTTTCTGTGTGAAATGTTATCGCTACA 2760
QY 2761 ATTCCACACAACATAGAGCGGAGAGCATTAAGTGTAAAGCTGTGGGTGCTTAATGAGTG 2820
Db 2761 ATTCCACACAACATAGAGCGGAGAGCATTAAGTGTAAAGCTGTGGGTGCTTAATGAGTG 2820
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Db 2821 AGCTAACTCACTAATATTTGGGTGCGCTCACTGCGCTTTCAGTGGGAAACCTGTG 2880
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Db 2881 TGCCAGCTGCAATTATGATGCGCAACGCGGGGGAGAGCGGTTTGCCTATTTGGCGC 2940
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Db 2941 TCTTCGCGCTTCTGCTCACTGACTGCGTGGCTCGGCTGCTTGGCTGCGCGAGCGGTA 3000
QY 3001 TCAGCTCACTGAAGCGGTATACGTTATTCACAGATGAGGGGATACGCAAGAAAG 3060
Db 3001 TCAGCTCACTGAAGCGGTATACGTTATTCACAGATGAGGGGATACGCAAGAAAG 3060
QY 3061 AACATGTAGCAAAAGGCGCAGCAAAAGGCCAGAAACGTTAAAAAAGCCGCTGTGCGC 3120
Db 3061 AACATGTAGCAAAAGGCGCAGCAAAAGGCCAGAAACGTTAAAAAAGCCGCTGTGCGC 3120
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Db 3181 TGGGAAAACCCGACAGAGACTATAAAGATCCAGGCGTTTCCCTGGAAGCTCCCTG 3240
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Db 3601 ACCTTCGAAAAGAGTGTGATGCTCTTGAATCCGGCAAAACACCGCTGTAGCGGT 3660
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Db 3661 GGTTTTTTTTGTGCAAGCAGAGATTACGCGCAGAAAAGAAATCTCAAGAAATCT 3720
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QY 3961 AGCCCGGGGTGGCGAAGAACTCAGCATGAGATCCCGGCTGGAAGATCATCGAGCG 4020
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QY 4021 GCGTCCCGGAAAACGATTCGGAAGCCCACTTTCATAGAAAGCGCGGTGGAATGAAA 4080
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QY 4081 TCTGTGATGAGCAGTTGGGCGTGGCTTGGTGGTCAATTCGAACCCAGAGTCCGCTC 4140
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Db      ||| 4081 TCTGTGATGGCAGGTTGGGGGTGCTTGTGTCGATCTTTCGAAACCCCAAGTCCCGCTC 4140
Qy      ||| 4141 AGAAGAACTGTCAAGAAAGCGATAGAAAGCGATGCGCTCGAATCGGAGCGCGCATAC 4200
Db      ||| 4141 AGAAGAACTGTCAAGAAAGCGATAGAAAGCGATGCGCTCGAATCGGAGCGCGCATAC 4200
Qy      ||| 4201 CGTAAAGCAGAGGAGCGGATGAGCGCATTCGCGCGCAAGCTCTTCAGCAATATCAAGGG 4260
Db      ||| 4201 GGTAAAGCAGAGGAGCGGATGAGCGCATTCGCGCGCAAGCTCTTCAGCAATATCAAGGG 4260
Qy      ||| 4261 TAGCCAAACGCTATGTCCTGATAGCGATCGCGCACACCCAGCGCGCACAGTCGATGATC 4320
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Qy      ||| 4441 GCCCTGATGCTCTTCTGTCAGATCATCTGATCGACAAAGCAGGCTTCATCCGAGTAC 4500
Db      ||| 4441 GCCCTGATGCTCTTCTGTCAGATCATCTGATCGACAAAGCAGGCTTCATCCGAGTAC 4500
Qy      ||| 4501 GTGCTGCTGATGATGCGATGTTTGGCTTGTGTGTGAATGGGAGAGTAGCCGATCAAGCG 4560
Db      ||| 4501 GTGCTGCTGATGATGCGATGTTTGGCTTGTGTGTGAATGGGAGAGTAGCCGATCAAGCG 4560
Qy      ||| 4561 TATGACAGCCGCGCATTTGATCATGACCATGATGATGATCTTTCTGCGGACGAGCAAGGTG 4620
Db      ||| 4561 TATGACAGCCGCGCATTTGATCATGACCATGATGATGATCTTTCTGCGGACGAGCAAGGTG 4620
Qy      ||| 4621 ATGACAGAGATCTGCGCGCGGACCTTGCGCCAAATAGCAGCAAGTCCCTTCCGCTTCA 4680
Db      ||| 4621 ATGACAGAGATCTGCGCGCGGACCTTGCGCCAAATAGCAGCAAGTCCCTTCCGCTTCA 4680
Qy      ||| 4681 TGAACAAGTGAAGCAGCTGCGCAAGAAAGCGCGCTGTGGCGACGACAGATAGCCGCG 4740
Db      ||| 4681 TGAACAAGTGAAGCAGCTGCGCAAGAAAGCGCGCTGTGGCGACGACAGATAGCCGCG 4740
Qy      ||| 4741 CTGCTGCTGCTGATGATTCATTCAGGGCACCGGACAGGTGCTTGAACAAAAGAACCG 4800
Db      ||| 4741 CTGCTGCTGCTGATGATTCATTCAGGGCACCGGACAGGTGCTTGAACAAAAGAACCG 4800
Qy      ||| 4801 GGGCGCCCTGCGCTGACAGCGCGGAAACCGCGGATCAGAGCCGATGCTGTGTG 4860
Db      ||| 4801 GGGCGCCCTGCGCTGACAGCGCGGAAACCGCGGATCAGAGCCGATGCTGTGTG 4860
Qy      ||| 4861 CCCAGTATAGCGGAATAGGCTCTCCACCCAAAGGCGCGGAAACCTGCGGCAATCAT 4920
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Qy      ||| 4921 CTGTTCATATCATGCGAAAGCATCTGATCTGTCTTGTATCATGATCTTGTATCCCTGC 4980
Db      ||| 4921 CTGTTCATATCATGCGAAAGCATCTGATCTGTCTTGTATCATGATCTTGTATCCCTGC 4980
Qy      ||| 4981 GCCATCATGATCTTGGGCGGCAAGAAAGCATCCAGTTTACTTTGAGGGCTTCCAACT 5040
Db      ||| 4981 GCCATCATGATCTTGGGCGGCAAGAAAGCATCCAGTTTACTTTGAGGGCTTCCAACT 5040
Qy      ||| 5041 TACCAAGAGGCGCGCCAGCTGCGCAATTCGCGTTGCTGTCATATAAAACCGCCAGT 5100
Db      ||| 5041 TACCAAGAGGCGCGCCAGCTGCGCAATTCGCGTTGCTGTCATATAAAACCGCCAGT 5100
Qy      ||| 5101 CTAGCTATGCGCATGTAAGCCCATCTGCAAGCTACTCTTCTTCTTTCGCTTGCCTTT 5160
Db      ||| 5101 CTAGCTATGCGCATGTAAGCCCATCTGCAAGCTACTCTTCTTCTTTCGCTTGCCTTT 5160
Qy      ||| 5161 CCTTGTTCAGATAGCCAGTAGCTGACATTCAGCGGGTCAGCACCGTTTCTGCGGAC 5220
Db      ||| 5161 CCTTGTTCAGATAGCCAGTAGCTGACATTCAGCGGGTCAGCACCGTTTCTGCGGAC 5220
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Db      ||| 5161 CCTTGTTCAGATAGCCAGTAGCTGACATTCAGCGGGTCAGCACCGTTTCTGCGGAC 5220
Qy      ||| 5221 TGGCTTTCTACGATGTTCCGCTTCTTTAGCAGGCTTGGCGCCTTAGATGTTTCCGCGAC 5280
Db      ||| 5221 TGGCTTTCTACGATGTTCCGCTTCTTTAGCAGGCTTGGCGCCTTAGATGTTTCCGCGAC 5280
Qy      ||| 5281 GTG 5283
Db      ||| 5281 GTG 5283

RESULT 2
AA15565
ID AA15565 standard; DNA; 8349 BP.
XX
AC AA15565;
XX
DT 28-JUL-2000 (first entry)
XX
DE PMON30464 plasmid.
XX
KM Transgenic plant; insect resistance; cry2a delta-endotoxin; Coleopteran;
KM Lepidopteran; Dipteran; plasmid transi peptide; zmsu PTP; insecticidal;
KM plasmid targeting peptide; PMON30464 plasmid; expression vector; ds.
XX
OS Synthetic.
XX
PN W0200026371-A1.
XX
PD 11-MAY-2000.
XX
PF 04-NOV-1999; 99MO-US026086.
XX
PR 04-NOV-1998; 98US-00186002.
XX
PA (MONS ) MONSANTO CO.
XX
PI Corbin DR, Romano CP;
XX
DR WPI; 2000-376130/32.
XX
PT New method of expressing insecticidal proteins in plants transformed with
PT a Bacillus thuringiensis delta-endotoxin encoding gene resulting in
PT effective control of susceptible target pests.
XX
PS Example 1; Page 96-99; 104pp; English.
XX
CC Bacillus thuringiensis produce delta-endotoxins during sporulation. These
CC proteins are toxic to certain insects e.g. Lepidopteran and Coleopteran
CC larvae. An insect-resistant transgenic plant has been constructed which
CC contains the delta-endotoxin cry2Ab gene. The present sequence would be
CC used to transfer delta-endotoxin genes into plant cells and for
CC subsequent high expression of the cry2Ab gene. Protection may be attained
CC against insects such as Ostrina spp., Diatraea spp., Helioverpa spp.,
CC and Spodoptera spp., in Zea mays; Heliothis virescens, Helicoverpa spp.,
CC Pectinophora spp., in Gossypium hirsutum; Anticarsa spp., Pseudoplusia
CC spp., Epinotia spp., in Glycine max; and Scirpophaga incertulas in Oryza
CC sativa. Expression of the endotoxin by a plant cell produces a fusion
CC protein comprising an amino-terminal plasmid transi peptide (zmsu PTP)
CC covalently linked to the delta-endotoxin. The fusion protein functions to
CC localise the delta-endotoxin to a subcellular organelle or compartment
XX
XX
Sequence 8349 BP; 1959 A; 2355 C; 2088 G; 1947 T; 0 U; 0 Other;
Query Match 42.4%; Score 2240; DB 3; Length 8349;
Best Local Similarity 93.4%; Pred. No. 0;
Matches 2409; Conservative 0; Mismatches 25; Indels 144; Gaps 1;
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Db 5971 ACACACATACGAGCCGGAAGCATAAAGTAAACCTGGGGTGCCTATGATGAGCTA 6030  
Qy 2826 ACTCATATTAAATTGGTTGCGCTCACTGCGCCGCTTTCAGTGGGAAAACCTTCCGTC 2885  
Db 6031 ACTCATATTAAATTGGTTGCGCTCACTGCGCCGCTTTCAGTGGGAAAACCTTCCGTC 6090  
Qy 2886 GCTGCATTAATGAATCGGCCAAACGCGCGGGAGAGCGGTTTGCATTTGGCGCTCTTC 2945  
Db 6091 GCTGCATTAATGAATCGGCCAAACGCGCGGGAGAGCGGTTTGCATTTGGCGCTCTTC 6150  
Qy 2946 GCTTTCCTCGCTCACTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3005  
Db 6151 GCTTTCCTCGCTCACTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6210  
Qy 3006 TCACCTCAAGGCGGTAAATACGGTTATCCAGAAATCAGAGGAGTAAACGAGGAAACAT 3065  
Db 6211 TCACCTCAAGGCGGTAAATACGGTTATCCAGAAATCAGAGGAGTAAACGAGGAAACAT 6270  
Qy 3066 GTGAGCAAAAGGCGCAAAAGGCGGAGAACCGTAAAGGCGGCTGCTGCTGCTT 3125  
Db 6271 GTGAGCAAAAGGCGCAAAAGGCGGAGAACCGTAAAGGCGGCTGCTGCTGCTT 6330  
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Db 6331 CCATAGGCTCCGCCCCCTGACGAGCATCAAAAATGACGCTCAAGTCAAGGTGCG 6390  
Qy 3186 AACCCGACAGAGCTATTAAGTATACAGGCGTTTCCCGTGAAGTCCCTCGGCTC 3245  
Db 6391 AACCCGACAGAGCTATTAAGTATACAGGCGTTTCCCGTGAAGTCCCTCGGCTC 6450  
Qy 3246 TCCTGTTCCGACCGCTGCGCTTACCGGATACCTGCTGCTTCCCTTGGGAGCGT 3305  
Db 6451 TCCTGTTCCGACCGCTGCGCTTACCGGATACCTGCTGCTTCCCTTGGGAGCGT 6510  
Qy 3306 GCGCCCTTCTAATAGCTACCGCTGATGCTGATGCTGATGCTGATGCTGCTGCT 3365  
Db 6511 GCGCCCTTCTAATAGCTACCGCTGATGCTGATGCTGATGCTGATGCTGCTGCT 6570  
Qy 3366 GCTGGGCTGTTGTCAGCAACCCCGCTTACGCGGACCGGCTGCTGCTGCTGCTGCT 3425  
Db 6571 GCTGGGCTGTTGTCAGCAACCCCGCTTACGCGGACCGGCTGCTGCTGCTGCTGCT 6630  
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Db 6631 TCCTGTTGAGTCCAAACCGGTAAGACACTTATCCGCACTGCGACGACCACTGTA 6690  
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Qy 3546 CTAAGGCTACACTGAGAGAACAGATTTGTAATGCTGCTGCTGCTGCTGCTGCTGCT 3605  
Db 6751 CTAAGGCTACACTGAGAGAACAGATTTGTAATGCTGCTGCTGCTGCTGCTGCTGCT 6810  
Qy 3606 CGGAAAAAGATTGTAAGTCTTGTATCCGCAACCAACGCTGCTGCTGCTGCTGCT 3665  
Db 6811 CGGAAAAAGATTGTAAGTCTTGTATCCGCAACCAACGCTGCTGCTGCTGCTGCT 6870  
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Db 6871 TTTTGTGTCAGAGCAGATTAACGCGAGAAAAAGATCTTCAAGAGATCTTTGAT 6930  
Qy 3726 CTTTTCACGAGGCTGACGCTCAGTGAAGAAATCAAGTAAAGATTTGGTCAT 3785  
Db 6931 CTTTTCACGAGGCTGACGCTCAGTGAAGAAATCAAGTAAAGATTTGGTCAT 6990  
Qy 3786 GAGATTATCGTCGACCAAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3845  
Db 6991 GAGATTATCGTCGACCAAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7024  
Qy 3846 GATGCGGAGATAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3905

Db 7025 ----- 7024  
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Db 7025 -----TT 7026  
Qy 3966 GGGGTGGCGAAGAACTTCAGATGAGATCCCGGCTGAGAGATCATTCAGCCGCGCTC 4025  
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Qy 4206 AGCAGAGAAAGCGGTCAAGCCCAATTGCGCGCAAGCTTTCAAGCAATATCAAGGATGCC 4265  
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Qy 4266 AACGCTATGCTCTGATGAGCGGTCCGCAACCCAGCGGCGCAAGTGAATTCAGAA 4325  
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Qy 4326 AAGCGGCAATTTTCCACATGATATTTGCGCAAGGAGATCGCCATGGGTCAAGACGAA 4385  
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DB 10128 CTTTTCCTACCGGAGTCTGAACGCTCAGTGAACGAAAACTCAGTTAAGGATTTTGTGAT 10187  
QY 3786 GAGATTATTCGTGACCAAAAGGGGCGCATGCTGCCACTTCCTGCAATTGGGGGCGATG 3845  
DB 10188 GAGATTATTCAAAAAAGGATCTTCACTAGATCCTT----- 10221  
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DB 10222 ----- 10221  
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DB 10584 AAGGCGCCATTTTCCACATGATATTCGGCAAGGCGATCGCATGGGTCAACGACGAGA 10643  
QY 4386 TCCCTCGCGTGGGCGATGCGCGCTTTAGCCTGGCGAAACGATTGGCTGGCGCGAGCCCC 4445  
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DB 10824 AGCGCGCGCATTTGATGAGCATGAGCATGATATCTTTCTCGGCGAGGACAAAGTGAATGAC 10883

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DB 11004 TCGTCTGCACTTCAATTCAGGGCAACCGGACAGTCCGCTTGAACAAAAAGAACCGGGGCG 11063  
QY 4806 CCTGCGCTGACAGCCCGGAAACAGCGGCGCATCAGAGCCGATTTGCTGTTGGCCAG 4865  
DB 11064 CCTGCGCTGACAGCCCGGAAACAGCGGCGCATCAGAGCCGATTTGCTGTTGGCCAG 11123  
QY 4866 TCATAGCCGAATAGCCTTCTCAACCCAGCGGCGGAGAACTGCGTGCATTCATTTGT 4925  
DB 11124 TCATAGCCGAATAGCCTTCTCAACCCAGCGGCGGAGAACTGCGTGCATTCATTTGT 11183  
QY 4926 TCATAGCCGAATAGCCTTCTCAACCCAGCGGCGGAGAACTGCGTGCATTCATTTGT 4985  
DB 11184 TCATAGCCGAATAGCCTTCTCAACCCAGCGGCGGAGAACTGCGTGCATTCATTTGT 11243  
QY 4986 CAGATCCTTGGCGGCAAGAAAGCCATCAGTTACTTTGCGAGGCTTCCCAACCTTACCA 5045  
DB 11244 CAGATCCTTGGCGGCAAGAAAGCCATCAGTTACTTTGCGAGGCTTCCCAACCTTACCA 11303  
QY 5046 GAGGCGCCCGCAAGCTGCAATTCGAGTTCGCTTGCCTGCTGCAATAAACCGCCAGTTCAGC 5105  
DB 11304 GAGGCGCCCGCAAGCTGCAATTCGAGTTCGCTTGCCTGCTGCAATAAACCGCCAGTTCAGC 11363  
QY 5106 TATGCGCATGTAAGCCCACTGCAAGCTACTGCTTTCTCTTGGCGTTCGCTTTCCCTT 5165  
DB 11364 TATGCGCATGTAAGCCCACTGCAAGCTACTGCTTTCTCTTGGCGTTCGCTTTCCCTT 11423  
QY 5166 GTCCAGATAGCCCGAGTGTGATGATCATTCGAGGCGTTCAGACCGCTTCTGCGAGTGGCT 5225  
DB 11424 GTCCAGATAGCCCGAGTGTGATGATCATTCGAGGCGTTCAGACCGCTTCTGCGAGTGGCT 11483  
QY 5226 TTCTACGTTGTCGCTTCTCTTTCAGACCCCTTGCGCCCTGAGTCTTTCGCGACGCTG 5283  
DB 11484 TTCTACGTTGTCGCTTCTCTTTCAGACCCCTTGCGCCCTGAGTCTTTCGCGACGCTG 11541

RESULT 4  
AAV29673/c  
ID AAV29673 standard; cDNA; 6136 BP.  
XX  
AC AAV29673;  
XX  
DT 01-SEP-1998 (first entry)  
XX  
DE Hybrid NAMK.6 (termyl-1-linker-CBDEGV) nucleotide sequence.  
XX  
KW Search; liquefaction; sweetener; enzyme hybrid; endoglycanase; enzyme;  
KW cellulose binding domain; CBD; starch processing; alpha-amylase;  
KW saccharification; Termyl-1-linker-CBD fusion; ss.  
XX  
OS *Bacillus* sp.  
XX  
OS *Humicola insolens*.  
XX  
PN W09816633-A1.  
XX  
PD 23-APR-1998.  
XX  
PF 13-OCT-1997; 97MO-DK000446.  
XX  
PR 11-OCT-1996; 96DK-00001130.  
XX  
PA (NOVO) NOVO-NORDISK AS.  
XX  
PI Bjornvad M, Pedersen S, Schuilein M, Biegaardfrantzen H;

XX WP1; 1998-251283/22.

XX Liquefaction of starch for, e.g. production of sweeteners - comprises use  
PT of enzyme hybrids including cellulose binding domain for starch.

XX Example 8, Page 65-67; 83pp; English.

XX This is the nucleotide sequence of the termamyl-linker-CBDEGV fusion  
XX construct pNBMK6.1. This is an enzyme hybrid which can be used for the  
CC liquefaction of starch. The enzyme hybrids contain amino acid sequences  
CC of alpha-amylase linked to a cellulose binding domain (CBD). The CBD is  
CC selected from the Bacillus or Cellulomonas endoglucanase, C. xylanase A  
CC or the Humicola insolens BGV sequence. The starch is liquefied by  
CC treating, in aqueous medium, with such an enzyme hybrid. A recombinant  
CC expression vector comprising a construct containing isolated DNA encoding  
CC enzyme hybrids with amylolytic activity, promoter and stop signals can be  
CC used to transform host cells for the production of the recombinant enzyme  
CC hybrids. The enzyme hybrids are useful in industrial starch processing  
CC especially for the production of sweeteners. Hybrid enzymes have altered  
CC affinity for substrate and increased activity, resulting in at least 1 of  
CC reduced calcium ion dependence, reduced formation of Maillard reaction  
CC products and reduced effect of alpha-amylase on subsequent  
CC saccharification

XX Sequence 6136 BP; 1475 A; 1545 C; 1712 G; 1404 T; 0 U; 0 Other;

XX Query Match 38.2%; Score 2017.2; DB 2; Length 6136;

XX Best Local Similarity 91.8%; Pred. No. 5.7e-297;

XX Matches 2203; Conservative 0; Mismatches 53; Indels 144; Gaps 1;

QY 2884 CAGCTGATTATGATCGGCAACGCGGGGAGAGCGGTTGGCTATGGCGGCT 2943  
DB 4381 CATATGCGGTGTGAATAACGACAGATCGTAAAGAAATACCGCATAGCGCTCT 4322  
QY 2944 TCCGGTCTCTGACTGACTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3003  
DB 4321 TCCGGTCTCTGACTGACTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4262  
QY 3004 GCTCACTCAAAAGCGGTATACCGTTATCAAGATCAAGGAGTAAACGACGAAAGAC 3063  
DB 4261 GCTCACTCAAAAGCGGTATACCGTTATCAAGATCAAGGAGTAAACGACGAAAGAC 4202  
QY 3064 ATGTACGAAAAAGCGACGAAAGCGGAAACGTTAAAGCGGCTGCTGCGCTT 3123  
DB 4201 ATGTACGAAAAAGCGACGAAAGCGGAAACGTTAAAGCGGCTGCTGCGCTT 4142  
QY 3124 TTCCATAGGCTCCGCCCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAAGGTGG 3183  
DB 4141 TTCCATAGGCTCCGCCCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAAGGTGG 4082  
QY 3184 CGAAACCGGACGAGCTATTAAGATACAGGCGGTTCCCTCGTGAAGCTCCCTGTGGC 3243  
DB 4081 CGAAACCGGACGAGCTATTAAGATACAGGCGGTTCCCTCGTGAAGCTCCCTGTGGC 4022  
QY 3244 TCTCTGTTCGACCTGCGCTTACCGGATACCTGTCGCTTCTCTGCGGAAAGC 3303  
DB 4021 TCTCTGTTCGACCTGCGCTTACCGGATACCTGTCGCTTCTCTGCGGAAAGC 3962  
QY 3304 GTGGGCTTTCATAGCTCAAGCTGTAGATCTCAAGTTCGCTGAGTGTGCTCC 3363  
DB 3961 GTGGGCTTTCATAGCTCAAGCTGTAGATCTCAAGTTCGCTGAGTGTGCTCC 3902  
QY 3364 AAGCTGGGTGTGTGACGAAACCCCGCTTACGCGCCGACCGGTGCGCTTACCGGTAC 3423  
DB 3901 AAGCTGGGTGTGTGACGAAACCCCGCTTACGCGCCGACCGGTGCGCTTACCGGTAC 3842  
QY 3424 TATCGCTTGAATCAACCGGTGAAGACGACTTATGCGCACTGGACGACCACTGGT 3483  
DB 3841 TATCGCTTGAATCAACCGGTGAAGACGACTTATGCGCACTGGACGACCACTGGT 3782  
QY 3484 AACAGATTAGACGAGCGATATGAGCGGTGCTACAGAGTTTGAAGTGTGGCT 3543

DB 3781 AACAGATTAGACGAGCGATATGAGCGGTGCTACAGAGTTCTTGAAGTGTGGCT 3722  
QY 3544 AACTACGCTACACTAGAAAGACATATTTGGTATCTGCGCTCTGCTCAACCGATTAC 3603  
DB 3721 AACTACGCTACACTAGAAAGACATATTTGGTATCTGCGCTCTGCTCAACCGATTAC 3662  
QY 3604 TTGGAAAAAGGTTGATAGCTTGTATCCGCAACAAACACCGCTGTAGCGGTGT 3663  
DB 3661 TTGGAAAAAGGTTGATAGCTTGTATCCGCAACAAACACCGCTGTAGCGGTGT 3602  
QY 3664 TTTTGTGTGTGACAGACAGATTAACGCGACAGAAAAAGATCTCAAGAAATCTTTG 3723  
DB 3601 TTTTGTGTGTGACAGACAGATTAACGCGACAGAAAAAGATCTCAAGAAATCTTTG 3542  
QY 3724 ATCTTTTTCAGCGGTCTGACGCTCAAGTGAACGAAACCTCAAGTGAAGTTGGTC 3783  
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QY 3784 ATGAGATTATCGTCGACCAACCGGCAATCTGCTCCCACTCTCGCATGTTGCGGGCA 3843  
DB 3481 ATGAGATTATCAAAAAAGATCTTCACTAGATCTT----- 3446  
QY 3844 TGGATGCGGATAGCGCGCTGCTGTTCTGGAATCCGACGGAATTTGCACTGCGGTAG 3903  
DB 3445 ----- 3446  
QY 3904 AACTCCGAGGTCGTCCAGCTCAGGACGAGCTGAACCAACTCGGAGGGATCGAC 3963  
DB 3445 ----- 3446  
QY 3964 CCGGGGTGGCGAAGAACTCAGCATGAGATCCCGCGCTGAGAGATCATCCAGCCGCG 4023  
DB 3445 TTGGGGTGGCGAAGAACTCAGCATGAGATCCCGCGCTGAGAGATCATCCAGCCGCG 3386  
QY 4024 TCCCGAAAAACGATTCGGAAGCCCACTTTATGAAGCGCGGTGAATTCGAATCT 4083  
DB 3385 TCCCGAAAAACGATTCGGAAGCCCACTTTATGAAGCGCGGTGAATTCGAATCT 3326  
QY 4084 CGTATGAGCAGGTGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4143  
DB 3325 CGTATGAGCAGGTGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3266  
QY 4144 AGAATCTGTCAAGAGCGATAGAGGCGATGCGCTGCGAATCGGAGCGGATTCGCT 4203  
DB 3265 AGAATCTGTCAAGAGCGATAGAGGCGATGCGCTGCGAATCGGAGCGGATTCGCT 3206  
QY 4204 AAGGACAGGAAGCGGTCAGCCCATTCGCGCGCAAGCTCTTCAAGATATCAAGGTTAG 4263  
DB 3205 AAGGACAGGAAGCGGTCAGCCCATTCGCGCGCAAGCTCTTCAAGATATCAAGGTTAG 3146  
QY 4264 CCAAGCTATGTCCTATAGCGGTCCGCAACCCAGCGGCAAGTGTGATTCAG 4323  
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QY 4324 AAAAGCGGCAATTTTCCACATATATTTGGCAAGGATATGCGATGGGTTCACAGCA 4383  
DB 3085 AAAAGCGGCAATTTTCCACATATATTTGGCAAGGATATGCGATGGGTTCACAGCA 3026  
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DB 3025 GATCTTCGCGGTGGGATGCGCGCTTGAAGCTTGAAGCAAGTTCGCGTGGCGAGGC 2966  
QY 4444 CCGTATGCTCTTGTCCATGATCTCTGATCGAACAGCGGCTTCATTCGATACGTG 4503  
DB 2965 CCGTATGCTCTTGTCCATGATCTCTGATCGAACAGCGGCTTCATTCGATACGTG 2906  
QY 4504 CTGCTCGATGCGATGTTTGTGCTTGTGTGCTGATATGGGAGGATACCGGATCAAGGAT 4563  
DB 2905 CTGCTCGATGCGATGTTTGTGCTTGTGTGCTGATATGGGAGGATACCGGATCAAGGAT 2846  
QY 4564 GCGAGCGCGCAATGATCATGAGCATGATGATCTTCTTCTGCGAGGACGAAGGTGATG 4623  
DB 2845 GCGAGCGCGCAATGATCATGAGCATGATGATCTTCTTCTGCGAGGACGAAGGTGATG 2786



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QY 3727 TTTTCTACGGGGCTCTGACGCTCACTGGAACGAAAACTCACGTTAAGGAATTTTGTCATG 3786
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Db 4200 TTTTCTACGGGGCTCTGACGCTCACTGGAACGAAAACTCACGTTAAGGAATTTTGTCAT- 4142
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QY 3787 AGATTATCGTCGACCAAGCGGCGCATCGTCCCTCCCACTCTGCAAGTTGGGGGCGATGG 3846
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Db 4141 ----- 4142
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QY 3847 ATGCGCGGATAGCCGCTGCTGTTTCTGTGATGCCAGCGATTGTGCACTGCGGTAGAAC 3906
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Db 4141 ----- 4142
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QY 3907 TCCGCGAGTTCGTCAGCCTCAGGCGACGAGCTGAACCACTCCGCGAGGGATGAGCCCG 3966
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Db 4141 -----9CCCC 4137
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QY 3967 GGGTGGGCGAAGAACTCCAGCATGAGATCCCGCGCTGAGAGATCATCCAGCCGGGCTCC 4026
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QY 4027 CGGAAAAAGATTTCGAAAGCCCACTTTCTAGAAAGCGGCGGTGGAATCGAAATCTCGT 4086
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|
Db 4076 CGGAAAAAGATTTCGAAAGCCCACTTTCTAGAAAGCGGCGGTGGAATCGAAATCTCGT 4017
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QY 4087 GATGCGAGTGGGGCGTCCGTTGGTGGTCAATTTCCAAACCCGAGTCCCGCTCAGAAAG 4146
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QY 4447 GATGCTCTTGTGCAAGTCACTCTGATCGACAGACCGGCTTCATCCGAGTACGTGCTC 4506
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Db 3656 GATGCTCTTGTGCAAGTCACTCTGATCGACAGACCGGCTTCATCCGAGTACGTGCTC 3597
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QY 4507 GCTCGATGCGATGTTTGGTTGGTGTCAATGGGCGAGTAGCCGATCAAGCGTATGCA 4566
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Db 3596 GCTCGATGCGATGTTTGGTTGGTGTGCAATGGGCGAGTAGCCGATCAAGCGTATGCA 3537
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QY 4807 CCTGCGCTGACGACCGCGAAACAGCGGCGCATCGAGACGCCATGTGCTGTGACCAGT 4866
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Db 2876 TCTACGTGTTCCGCTTCTTTAGCAGCCCTTGCAGGTGCTTGCAGGACGCTG 2820
|
|
|
FT

RESULT 6
ADT55139
ID ADT55139 standard; DNA; 4058 BP.
XX
AC ADT55139;
XX
DT 30-DEC-2004 (first entry)
XX
DE Nucleotide sequence of expression vector pMB1-hiFna1pha.
XX
KW Ophthalmological; radiation; free radical; superoxide dismutase; anion;
KW heavy metal cation; metallochionein; superoxide dismutase; SOD; catalase;
KW glutathione peroxidase 4; GPX-4; gamma glutamyl transpeptidase;
KW xeroderma; xeroderma; autoimmune disorder; Sjogren's syndrome;
KW graft-versus-host disease; systemic lupus erythematosus;
KW rheumatoid arthritis; HIV-1 infection; ageing; autonomic dysfunction;
KW psychogenic disorder; trauma; hepatitis C; cancer; mastectomy; ss.
XX
OS Homo sapiens.
OS Simian virus 40.
OS Synthetic.
XX
FH Key location/Qualifiers
FT intron 332..497
FT /tag= a
FT /note= "human beta-globin intron"
FT polyA_signal 347..503
FT /tag= b
FT /note= "SV40 late gene polyadenylation signal"
FT promoter 471..1162
FT /tag= c
FT /note= "CMV promoter"
FT CDS 551..1077
FT /tag= d
FT /note= "human interferon (IFN) alpha cDNA"
FT rep_origin 1158..1825
FT /tag= e
FT /note= "ColEI ori from pBluescript SK+"
FT CDS 1226..2020
FT /tag= f
FT
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QY 3006 TCACTCAAAAGGCGGTAAATACGGTTATCCACAGAAATCAGGGGATAACGCAAGGAAAGAAACAT 3065  
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QY 3066 GTGAGCAAAAGGCGCAAGCAAAAGGCGCAAGCAACCGTAAAAAGGCGCGTTGCTGGCGCTTTT 3125  
Db 2466 GTGAGCAAAAGGCGCAAGCAAAAGGCGCAAGCAACCGTAAAAAGGCGCGTTGCTGGCGCTTTT 2525  
QY 3126 CCATAGGCTCGGCCCCCTGACGAGCATCACAAAAATGACGCTCAATTCAGAGGTGGCG 3185  
Db 2526 CCATAGGCTCGGCCCCCTGACGAGCATCACAAAAATGACGCTCAATTCAGAGGTGGCG 2585  
QY 3186 AAACCCGACAGAGACTATTAAGATACAGAGCTTTCCCTGGAAAGCTCCCTGATGCGCTC 3245  
Db 2586 AAACCCGACAGAGACTATTAAGATACAGAGCTTTCCCTGGAAAGCTCCCTGATGCGCTC 2645  
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QY 3306 GGCCCTTTCTATAGCTCAAGCTGTAGGTATCTCAGTTGCGTTAGGTGCTTCCCTCAA 3365  
Db 2706 GGCCCTTTCTATAGCTCAAGCTGTAGGTATCTCAGTTGCGTTAGGTGCTTCCCTCAA 2765  
QY 3366 GCTGGGCTGTGACGAAACCCCGTTACAGCCGACCGCTGCGCTTATCCGGAATCA 3425  
Db 2766 GCTGGGCTGTGACGAAACCCCGTTACAGCCGACCGCTGCGCTTATCCGGAATCA 2825  
QY 3426 TCGCTTTGAGTCCAAACCGGTAGACACAGCTTATCCGCACTGGACAGCAGCACTGTAA 3485  
Db 2826 TCGCTTTGAGTCCAAACCGGTAGACACAGCTTATCCGCACTGGACAGCAGCACTGTAA 2885  
QY 3486 CAGATTTAGCAGACGAGGTATGTAGGGGCTGCTACAGATTTCTTGAAGTGTGCTTAA 3545  
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QY 3546 CTACGGCTACACAGAAAGCAAGTATTTGATCTGCGCTGCTGCAAGCAAGTAACTT 3605  
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QY 3606 CGGAAAAAGAGTTGTAGCTTGTATCCGCAAAACCAACCGCTGTAGCGGTGTT 3665  
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Db 3189 ----- 3188  
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Db 3345 AACTGTCAGAGGCGATAGAGGCGATGCGCTGCGAATCGGAGCGGCGATACCGTAA 3404  
QY 4206 AGCAGAGGAAGCGGTGAGCCCATTTCCCGGCAAGCTTTTACAGCAATATCAGGGTACC 4265  
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QY 4266 AACCTATGTCCTGATAGCGGTCCGCAACCCAGCGCGGCAAGTGCATGATATCAGAA 4325  
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QY 4326 AAGCGGCATTTTTCACCATGATATTCGCAAGAGGATGCCATGGGTACAGACGAGA 4385  
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QY 4386 TCCTGCGCGCTGGGCAATGCGGCTTGAAGCTGGCGAAACAGTTGCGCTGGCGGAGCCC 4445  
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QY 4446 TGATGCTCTTGTGTCAGATCATCCTGATCGAACAGACCGGCTTCCATCCGATACGTGCT 4505  
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QY 4506 CGCTCGATGCGATGTTTCGCTTGTGATCGAATGCGGAGGATGAGCGGATCAAGGATATG 4565  
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QY 4686 ACCTGAGCAACAGCTGCGCAAGAAACCCGTCGTGCGCAGCCAGATAGCGCGCTGCC 4745  
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QY 4746 TCGTCTGCAAGTTATTCAGGGCACCGGACAGGTGCTTGTACAAAAAGAACCGGGCGC 4805  
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QY 4986 CAG 4988  
Db 4185 CAG 4187  
  
RESULT 8  
ADT5136  
ID ADT5136 standard; DNA: 4293 BP.  
XX ADT5136;  
AC  
XX  
XX  
DT 30-DEC-2004 (first entry)  
XX

DE Nucleotide sequence of expression vector pMB1-HA-MnSOD.  
XX Ophthalmological; radiation; free radical; superoxide anion;  
XX heavy metal cation; metallothionein; superoxide dismutase; SOD; catalase;  
XX glutathione peroxidase 4; GPX-4; gamma glutamyl transpeptidase;  
XX xeroderma; xerophthalmia; autoimmune disorder; Sjogren's syndrome;  
XX graft-versus-host disease; systemic lupus erythematosus;  
XX rheumatoid arthritis; HIV-1 infection; ageing; autonomic dysfunction;  
XX psychogenic disorder; trauma; hepatitis C; cancer; mastication; se.  
XX Homo sapiens.  
OS Simian virus 40.  
OS Synthetic.  
XX Key Location/Qualifiers  
XX CDS 2..781  
XX /tag= a  
XX /note= "human Manganese superoxide dismutase cDNA"  
XX intron 332..497  
XX /tag= b  
XX /note= "human beta-globin intron"  
XX polyA\_signal 347..503  
XX /tag= c  
XX /note= "SV40 late gene polyadenylation signal"  
XX promoter 471..1162  
XX /tag= d  
XX /note= "CMV promoter"  
XX rep\_origin 1158..1825  
XX /tag= e  
XX /note= "ColE1 ori from pBluescript SK+"  
XX CDS 1226..2020  
XX /tag= f  
XX /gene= "kanamycin resistance gene"  
XX  
XX WO2004087873-A2.  
XX  
XX 14-OCT-2004.  
XX  
XX PD 26-MAR-2004; 2004WO-US009194.  
XX  
XX PR 26-MAR-2003; 2003US-0458793P.  
XX PR 25-MAR-2004; 2004US-0777889P.  
XX  
XX PA (GENT-) GENTERIC INC.  
XX  
XX PI Bennett MJ, Chen Y;  
XX  
XX WPI; 2004-737685/72.  
XX  
XX DR Attenuating increases in concentrations of radiation-induced free  
XX PT radicals in a mammalian cell, comprises contacting the cell with one or  
XX PT more nucleic acids encoding proteins that neutralizes or eliminates a  
XX PT portion of free radicals.  
XX  
XX PS Claim 34; SEQ ID NO 2; 58pp; English.  
XX  
XX The specification describes a method for attenuating increases in  
XX concentrations of radiation-induced free radicals, superoxide anions or  
XX heavy metal cations in a mammalian cell. The method comprises contacting  
XX the cell with one or more nucleic acids encoding one or more proteins  
XX that are expressed in the cell and that neutralizes or eliminates a  
XX portion of the free radicals, superoxide anions or heavy metal cations in  
XX the cell. The proteins are selected from metallothionein, superoxide  
XX dismutase, catalase, glutathione peroxidase (GPX)-4, or gamma glutamyl  
XX transpeptidase. The method is useful for attenuating increases in  
XX concentrations of radiation-induced free radicals, superoxide anions or  
XX heavy metal cations in a mammalian cell, and ameliorating symptoms of  
XX xeroderma or xerophthalmia associated with conditions such as autoimmune  
XX disorders, Sjogren's syndrome, graft-versus-host disease, systemic lupus  
XX erythematosus, rheumatoid arthritis, HIV-1 infection, ageing, autonomic  
XX dysfunction, conditions affecting the CNS, psychogenic disorder, trauma,  
XX hepatitis C, cancer and decrease in mastication. The present sequence  
XX represents an expression vector used in the method of the invention

CC express the relevant proteins.  
XX  
XX Sequence 4293 BP; 1089 A; 1090 C; 1112 G; 1001 T; 0 U; 1 Other;  
SQ  
Query Match 32.1%; Score 1697.8; DB 13; Length 4293;  
Best Local Similarity 86.7%; Pred. No. 1.5e-248;  
Matches 1980; Conservative 0; Mismatches 102; Indels 201; Gaps 2;  
QY 2706 CTAGACGTAATGATGCTACCTGTTCCCTGTGAAATTGTATCCGCTACAAATCC 2765  
DB 2212 CTTGGGTATATCATGCTCATGCTGTTCTCTGTGAATATGTATCCGCTCACATATCC 2271  
QY 2766 ACACAATATGACGCGGAGAGATTAAGTAAAGCTGGGCTATAGTAGCTA 2825  
DB 2272 ACACAATATGACGCGGAGAGATTAAGTAAAGCTGGGCTATAGTAGCTA 2331  
QY 2826 ACTCAATTATTTGCGTTCGCTCACTGCGCGCTTTCAGTGGGAAACCTTCGTGCCA 2885  
DB 2332 ACTCAATTATTTGCGTTCGCTCACTGCGCGCTTTCAGTGGGAAACCTTCGTGCCA 2391  
QY 2886 GCTGCAATTATGATGCGCAACGCGCGGAGAGCGGTTGCGATTTGGCGCTCTTC 2945  
DB 2392 GCTGCAATTATGATGCGCAACGCGCGGAGAGCGGTTGCGATTTGGCGCTCTTC 2451  
QY 2946 CGCTTCCTGCTCACTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3005  
DB 2452 CGCTTCCTGCTCACTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2511  
QY 3006 TCACTGAAAGGCGGTATATCGGTTATCCACAAATTCAGGGGATTAACGAGAAAGACAT 3065  
DB 2512 TCACTGAAAGGCGGTATATCGGTTATCCACAAATTCAGGGGATTAACGAGAAAGACAT 2571  
QY 3066 GTGAGCAAAAGGCGCAAAAGGCGCAAGACCGTAAAGGCGGCTTCGCGCTTTT 3125  
DB 2572 GTGAGCAAAAGGCGCAAAAGGCGCAAGACCGTAAAGGCGGCTTCGCGCTTTT 2631  
QY 3126 CCATAGGCTCCGCGCCCTGACGAGCATCAAAAATTCAGCGTCAAGTCAAGTGGCG 3185  
DB 2632 CCATAGGCTCCGCGCCCTGACGAGCATCAAAAATTCAGCGTCAAGTCAAGTGGCG 2691  
QY 3186 AAACCCGACAGGACTTAAAGATACAGAGGCTTCCCGTGAAGGCTCCCTGCGCTC 3245  
DB 2692 AAACCCGACAGGACTTAAAGATACAGAGGCTTCCCGTGAAGGCTCCCTGCGCTC 2751  
QY 3246 TCCTGTTCCGACCCCTGCTTACCGGATACCTGTCCGCTTCTCCTTCGGAAAGCGT 3305  
DB 2752 TCCTGTTCCGACCCCTGCTTACCGGATACCTGTCCGCTTCTCCTTCGGAAAGCGT 2811  
QY 3306 GCGGCTTCTCATAGCTCACGCTGTAGGTATCTCACTTGGGTAGTGGTTCGCTCCA 3365  
DB 2812 GCGGCTTCTCATAGCTCACGCTGTAGGTATCTCACTTGGGTAGTGGTTCGCTCCA 2871  
QY 3366 GCGGCTTCTCATAGCTCACGCTGTAGGTATCTCACTTGGGTAGTGGTTCGCTCCA 3425  
DB 2872 GCGGCTTCTCATAGCTCACGCTGTAGGTATCTCACTTGGGTAGTGGTTCGCTCCA 2931  
QY 3426 TCGCTTTGATCCCAACCCGCTTAAGACACGATTAATGCGCATGCGACGACCTGTAA 3485  
DB 2932 TCGCTTTGATCCCAACCCGCTTAAGACACGATTAATGCGCATGCGACGACCTGTAA 2991  
QY 3486 CAGGATTAAGACGAGGATTAAGGCGGTGTAGGCGGTGTAGGCGGTGTAGGCGGTAA 3545  
DB 2992 CAGGATTAAGACGAGGATTAAGGCGGTGTAGGCGGTGTAGGCGGTGTAGGCGGTAA 3051  
QY 3546 CTAAGGCTTACCTAGAAACAGATTAATTTGTATCTGCTCTGCTAGGCAAGCTTACCTT 3605  
DB 3052 CTAAGGCTTACCTAGAAACAGATTAATTTGTATCTGCTCTGCTAGGCAAGCTTACCTT 3111  
QY 3606 CGGAAAAAGGTTGATGCTTTGATTCGCAAAACCAACCGCTGTTAGCGGTGTT 3665  
DB 3112 CGGAAAAAGGTTGATGCTTTGATTCGCAAAACCAACCGCTGTTAGCGGTGTT 3171  
QY 3666 TTTTGTTCAGAGAGAGATTAAGCGGCAAAAAAGATTCAGAAAGATCTTTGAT 3725



XX  
DR WPI; 2004-737685/72.

PT Attenuating increases in concentrations of radiation-induced free  
PT radicals in a mammalian cell, comprises contacting the cell with one or  
PT more nucleic acids encoding proteins that neutralizes or eliminates a  
PT portion of free radicals.

PS Claim 34; SEQ ID NO 1; 58pp; English.

The specification describes a method for attenuating increases in concentrations of radiation-induced free radicals, superoxide anions or heavy metal cations in a mammalian cell. The method comprises contacting the cell with one or more nucleic acids encoding one or more proteins that are expressed in the cell and that neutralizes or eliminates a portion of the free radicals, superoxide anions or heavy metal cations in the cell. The proteins are selected from metallothionein, superoxide dismutase, catalase, glutathione peroxidase (GPx)-4, or gamma glutamyl transpeptidase. The method is useful for attenuating increases in concentrations of radiation-induced free radicals, superoxide anions or heavy metal cations in a mammalian cell, and ameliorating symptoms of xeroderma or xerophthalmia associated with conditions such as autoimmune disorders, Sjogren's syndrome, graft-versus-host disease, systemic lupus erythematosus, rheumatoid arthritis, HIV-1 infection, ageing, autonomic dysfunction, conditions affecting the CNS, psychogenic disorder, trauma, hepatitis C, cancer and decrease in mastication. The present sequence represents an expression vector used in the method of the invention to express the relevant proteins.

SQ Sequence 4332 BP; 1094 A; 1102 C; 1137 G; 998 T; 0 U; 1 Other;

Query Match	Score	DB	Length
32.1%	1697.8	13	4332

Best Local Similarity 86.7%; Pred. No. 1.5e-248;  
Matches 1980; Conservative 0; Mismatches 102; Indels 201; Gaps 22

QY	2706	CTAAGCGTAATCAATGATGATATAGCTGTTCCGTGTGAAATTTGTAATCCGCTCACAATATCC	2765S
Db	2251	CTTGGCGTAATCAATGATATAGCTGTTCCGTGTGAAATTTGTAATCCGCTCACAATATCC	2310U
QY	2766	ACACAACTACGAGCCGGAGCATTAAGTGTAAAGCCCTGGGGTGCCTATAGTAGCTA	2825S
Db	2311	ACACAACTACGAGCCGGAGCATTAAGTGTAAAGCCCTGGGGTGCCTATAGTAGCTA	2370U
QY	2826	ACTCAATTAATTTGGCTTGGCGCTCACTGCCCGCTTTCATGTGGGAAACCTGTGTCGA	2885S
Db	2371	ACTCAATTAATTTGGCTTGGCGCTCACTGCCCGCTTTCATGTGGGAAACCTGTGTCGA	2430U
QY	2886	GCTGCATTAATGAATCGGCACAAACGCGGGGAGAGCGGCTTTGGGTAATGGAGCGCTTTC	2945S
Db	2431	GCTGCATTAATGAATCGGCACAAACGCGGGGAGAGCGGCTTTGGGTAATGGAGCGCTTTC	2490U
QY	2946	CGCTTTCCTCGCTCACTGACTGCGTGGCGCTCGTGTGGCTGCGGACGAGCGATACGC	3005S
Db	2491	CGCTTTCCTCGCTCACTGACTGCGTGGCGCTCGTGTGGCTGCGGACGAGCGATACGC	2550U
QY	3006	TCACCTCAAAAGCGGTAATACGGTTATCCACAGAAATCAGGGATTAACGAGAGAAAGAACAT	3065S
Db	2551	TCACCTCAAAAGCGGTAATACGGTTATCCACAGAAATCAGGGATTAACGAGAGAAAGAACAT	2610U
QY	3066	GTGAGCAAAAAGCCAGCAAAAAGGCGCAGGAACCGTAAAAAAGGCCCGCTGTGCGGCTTTT	3125S
Db	2611	GTGAGCAAAAAGCCAGCAAAAAGGCGCAGGAACCGTAAAAAAGGCCCGCTGTGCGGCTTTT	2670U
QY	3126	CCATAGGCTCGGCCCTCTGACGAGCATCACAAAATATGACGCTCAAGTCAAGAGTGGCG	3185S
Db	2671	CCATAGGCTCGGCCCTCTGACGAGCATCACAAAATATGACGCTCAAGTCAAGAGTGGCG	2730U
QY	3186	AAACCCCAACAGCATTAATAAGATACAGAGGCTTTCCCTCTGGAAAGCTCCCTCGGCGCTC	3245S
Db	2731	AAACCCCAACAGCATTAATAAGATACAGAGGCTTTCCCTCTGGAAAGCTCCCTCGGCGCTC	2790U
QY	3246	TCCTGTTCGACCTCGGCGCTTACCGGATACCTGTCCGCTTTCTCCCTTTCGGAAACGT	3305S
Db		TCCTGTTCGACCTCGGCGCTTACCGGATACCTGTCCGCTTTCTCCCTTTCGGAAACGT	









RESULT 11  
ADT55138  
ID ADT55138 standard; DNA; 5760 BP.  
XX  
AC ADT55138;  
XX  
DT 30-DEC-2004 (first entry)  
XX  
XX Nucleotide sequence of expression vector pMB1-MtLocAT.  
XX  
KW Ophthalmological; radiation; free radical; superoxide anion;  
KW heavy metal cation; metallothionein; superoxide dismutase; SOD; catalase;  
KW glutathione peroxidase 4; Gpx-4; gamma glutamyl transpeptidase;  
KW xerostomia; xerophthalmia; autoimmune disorder; Sjogren's syndrome;  
KW graft-versus-host disease; systemic lupus erythematosus;  
KW rheumatoid arthritis; HIV-1 infection; ageing; autonomic dysfunction;  
KW psychogenic disorder; trauma; hepatitis C; cancer; mastication; ss.  
XX  
OS Homo sapiens.  
OS Simian virus 40.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT intron 332..497  
FT /tag= a  
FT /note= "human beta-globin intron"  
FT 345..503  
FT /tag= b  
FT /note= "SV40 late gene polyadenylation signal"  
FT 471..1162  
FT /tag= c  
FT /note= "human cytomegalovirus IE1 gene promoter region"  
FT 1100..1172  
FT /tag= d  
FT /note= "mitochondrial leader sequence"  
FT 1158..1825  
FT /tag= e  
FT /note= "ColE1 ori from pBluescript SK+"  
FT 1173..3419  
FT /tag= f  
FT /note= "encodes catalase"  
FT 1226..2020  
FT /tag= g  
FT /gene= "kanamycin resistance gene"  
XX  
PN W02004087873-A2.  
XX  
PD 14-OCT-2004.  
XX  
PF 26-MAR-2004; 2004WO-US009194.  
XX  
PR 26-MAR-2003; 2003US-0458793P.  
PR 25-MAR-2004; 2004US-07778889.  
XX  
PA (GENT-) GENTERIC INC.  
XX  
PI Bennett MJ, Chen Y;  
XX  
XX WPI; 2004-737685/72.  
XX  
XX Attenuating increases in concentrations of radiation-induced free  
XX radicals in a mammalian cell, comprises contacting the cell with one or  
XX more nucleic acids encoding proteins that neutralizes or eliminates a  
XX portion of free radicals.  
XX  
PS Claim 34; SEQ ID NO 4; 58pp; English.  
XX  
XX The specification describes a method for attenuating increases in  
XX concentrations of radiation-induced free radicals, superoxide anions or  
XX heavy metal cations in a mammalian cell. The method comprises contacting  
XX the cell with one or more nucleic acids encoding one or more proteins  
XX that are expressed in the cell and that neutralizes or eliminates a  
XX portion of the free radicals, superoxide anions or heavy metal cations in

CC the cell. The proteins are selected from metallothionein, superoxide  
CC dismutase, catalase, glutathione peroxidase (Gpx)-4, or gamma glutamyl  
CC transpeptidase. The method is useful for attenuating increases in  
CC concentrations of radiation-induced free radicals, superoxide anions or  
CC heavy metal cations in a mammalian cell, and ameliorating symptoms of  
CC xerostomia or xerophthalmia associated with conditions such as autoimmune  
CC disorders, Sjogren's syndrome, graft-versus-host disease, systemic lupus  
CC erythematosus, rheumatoid arthritis, HIV-1 infection, ageing, autonomic  
CC dysfunction, conditions affecting the CNS, psychogenic disorder, trauma,  
CC hepatitis C, cancer and decrease in mastication. The present sequence  
CC represents an expression vector used in the method of the invention to  
CC express the relevant proteins.  
XX  
SQ Sequence 5760 BP; 1471 A; 1422 C; 1426 G; 1441 T; 0 U; 0 Other;  
Query Match 32.1%; Score 1697.8; DB 13; Length 5760;  
Best Local Similarity 86.7%; Pred. No. 1.5e-248;  
Matches 1980; Conservative 0; Mismatches 102; Indels 201; Gaps 2;  
QY 2706 CTGACGTAATCATGTCATGCTGTTTCCGTGTAATGTTATCCGCTCACAAATCC 2765  
DB 3679 CTTGGCTTAATCATGTCATGCTGTTTCCGTGTAATGTTATCCGCTCACAAATCC 3738  
QY 2766 ACACAAATACGAGCCGGAACATTAAGTGTAAAGCTGGGCTCTTAATGATGAGCTA 2825  
DB 3739 ACACAAATACGAGCCGGAACATTAAGTGTAAAGCTGGGCTCTTAATGATGAGCTA 3798  
QY 2826 ACTCACTTAATTCGTTGCGCTCACTGCGCTTTTCCAGTCGGGAAAACCTGTGTCGA 2885  
DB 3799 ACTCACTTAATTCGTTGCGCTCACTGCGCTTTTCCAGTCGGGAAAACCTGTGTCGA 3858  
QY 2886 GCTGCATTAATGAATCGGCGCAAGCGCGGGAGAGGGGTTTGTTGTTGGGCGCTCTTC 2945  
DB 3859 GCTGCATTAATGAATCGGCGCAAGCGCGGGAGAGGGGTTTGTTGTTGGGCGCTCTTC 3918  
QY 2946 CGCTTCTCGCTCACTGACTGCGCTCGCTGTTTCCGCTGCGGAGAGGATATGACG 3005  
DB 3919 CGCTTCTCGCTCACTGACTGCGCTCGCTGTTTCCGCTGCGGAGAGGATATGACG 3978  
QY 3006 TCACCTAAAGGCGGTAATACGCTTATCAAGAAATACAGGAGTAACGAGAAAGAAAT 3065  
DB 3979 TCACCTAAAGGCGGTAATACGCTTATCAAGAAATACAGGAGTAACGAGAAAGAAAT 4038  
QY 3066 GTGAGCAAAAGGCGGCAAAAGCGGCAAAAGCGGCGGCTGCTGCGGCTTTT 3125  
DB 4039 GTGAGCAAAAGGCGGCAAAAGCGGCAAAAGCGGCGGCTGCTGCGGCTTTT 4098  
QY 3126 CCATGAGCTCGCGCCCGCTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGTGGCG 3185  
DB 4099 CCATGAGCTCGCGCCCGCTGACGAGCATCAAAAATCGACGCTCAAGTGGAGTGGCG 4158  
QY 3186 AAACCCGACAGACTAATAAGATACAGGCGGTTTCCCTGGAAGGCTCCCTGCGCTC 3245  
DB 4159 AAACCCGACAGACTAATAAGATACAGGCGGTTTCCCTGGAAGGCTCCCTGCGCTC 4218  
QY 3246 TCCGTTCCGACCCCTGCGCTTACCCGATACCTGTCGCTTTTCCCTTCGGGAACGCT 3305  
DB 4219 TCCGTTCCGACCCCTGCGCTTACCCGATACCTGTCGCTTTTCCCTTCGGGAACGCT 4278  
QY 3306 GCGGCTTCTCATAGCTCAGCGTGTAGTATTCAGTTGCGGTGAGTCTGCTCCAA 3365  
DB 4279 GCGGCTTCTCATAGCTCAGCGTGTAGTATTCAGTTGCGGTGAGTCTGCTCCAA 4338  
QY 3366 GCTGGGCTGTGTGACGAACCCCGCTTACGCCGACGCGTGGCTTATCCGTTAACTA 3425  
DB 4339 GCTGGGCTGTGTGACGAACCCCGCTTACGCCGACGCGTGGCTTATCCGTTAACTA 4398  
QY 3426 TCGCTTGAATCCAAACCGGTGTAAGACGACTTATGCGCACTGGGACGACCACTGGTAA 3485  
DB 4399 TCGCTTGAATCCAAACCGGTGTAAGACGACTTATGCGCACTGGGACGACCACTGGTAA 4458  
QY 3486 CAGGATTAGCAGACGAGATGTAGCGGTGCTACAGAGTTCTTGAAGTGGGCTTAA 3545

Db 4459 CAGATTAGCAGACGAGGATATGAGCGGTCTACAGAGTTCTTGAAGTGTGCTTAA 4518  
QY 3546 CTACGGCTACATAGAGAAAGATATTTGGTATCTGGCTCTGTGAAGCAAGTAACTT 3605  
Db 4519 CTACGGCTACATAGAGAAAGATATTTGGTATCTGGCTCTGTGAAGCAAGTAACTT 4578  
QY 3606 CGGAAAAAGGTTGTAGCTCTTGTATCCGGCAAAACAACCGCTGTGTGCGGTGTTT 3665  
Db 4579 CGGAAAAAGGTTGTAGCTCTTGTATCCGGCAAAACAACCGCTGTGTGCGGTGTTT 4638  
QY 3666 TTTTGTGTGAGAGCAGAGATTAACGCGAGAAAAAAGATCTCAAGAAATCCTTTGAT 3725  
Db 4639 TTTTGTGTGAGAGCAGAGATTAACGCGAGAAAAAAGATCTCAAGAAATCCTTTGAT 4698  
QY 3726 CTTTTCACGGGCTCTGACGCTCAGTGAAGAACTCAAGTTAAGGATTTTGTGAT 3785  
Db 4699 CTTTTCACGGGCTCTGACGCTCAGTGAAGAACTCAAGTTAAGGATTTTGTGAT 4758  
QY 3786 GAGATTATCGTCGACCAAGCGGCATCGTGTCTCCCACTCCCTGCAAGTTCCGGGGGATG 3845  
Db 4759 GAG----- 4761  
QY 3846 GATCGCGGATAGCGCTGTGTTCTCTGATGCCAGCGATTGCACTGCCGTAGAA 3905  
Db 4762 ----- 4761  
QY 3906 CTCGCGAGGTCGTCCAGCCTCAGGCGACAGCTGAACCACTCCGCGGGGATCGAGCCC 3965  
Db 4762 -----CGATACATATTTGATATTTAGAAAAATPAAACMAATAG 4802  
QY 3966 GGGGTGGCGAAGAACTCCAGCATGAGATCCCGCGTGAAGATCATCCAGCGGCGTC 4025  
Db 4803 GGGTTCGCGCACATTTCCCGAAAGTGCCACTGTATGCGGTGAATACCGCACAG 4862  
QY 4026 CCGGAAAAAGATTCGAAAGCCCAACTTTATAGAGCGCGGTGAATCGAAATCTCG 4085  
Db 4863 ATGGGTAGAGAAATATACCGCATCAGAAATTTGTAAGCGTTAATAAT----- 4910  
QY 4086 TGATGGCAGGTTGGGCGTGGTGTGTGATTTCCAAACCCAGAGTCCCGCTCAGAAAG 4145  
Db 4911 -----TCAGAAAG 4917  
QY 4146 AACTCGTCAAGAAAGCGATAGAAAGCGATGCGTGCATTCGGAAGCGGCGATACCGTAA 4205  
Db 4918 AACTCGTCAAGAAAGCGATAGAAAGCGATGCGTGCATTCGGAAGCGGCGATACCGTAA 4977  
QY 4206 AGCAGAGAGAAAGCGGTCAAGCCCATTCGCGCAAGCTCTTCAGCAATATCACGGTAAGCC 4265  
Db 4978 AGCAGAGAGAAAGCGGTCAAGCCCATTCGCGCGCAAGCTCTTCAGCAATATCACGGTAAGCC 5037  
QY 4266 AAGCGTATGCTCTGATAGCGGTCCGCCACACCGCGCGCAAGTGTGATGAATCCAGAA 4325  
Db 5038 AAGCGTATGCTCTGATAGCGGTCCGCCACACCGCGCGCAAGTGTGATGAATCCAGAA 5097  
QY 4326 AAGCGGCAATTTTCCACCATGATATTCGCAAGCAGCATGCGATGGGTCAACAGCAGA 4385  
Db 5098 AAGCGGCAATTTTCCACCATGATATTCGCAAGCAGCATGCGATGGGTCAACAGCAGA 5157  
QY 4386 TCCTCGCGGTGCGGATGCGCGCTTGAAGCTGCGCAACAGTTGCGTGGCGAGACCCC 4445  
Db 5158 TCCTCGCGGTGCGGATGCGCGCTTGAAGCTGCGCAACAGTTGCGTGGCGAGACCCC 5217  
QY 4446 TGATGCTCTTGTGTCAGATCATCTGATCGACAGACCGGTTTCATCCGAGTACGATGCT 4505  
Db 5218 TGATGCTCTTGTGTCAGATCATCTGATCGACAGACCGGTTTCATCCGAGTACGATGCT 5277  
QY 4506 CGCTCGATGCGATTTTGCCTGGTGGTGCATGAGGAGGAGTGAAGCGATATGCG 4565  
Db 5278 CGCTCGATGCGATTTTGCCTGGTGGTGCATGAGGAGGAGTGAAGCGATATGCG 5337  
QY 4566 AGCGCGCGCATTCATCAGCCCATGATGATCTTTCTCGCGAGAGCAAGGTGATGATC 4625  
Db 5338 AGCGCGCGCATTCATCAGCCCATGATGATCTTTCTCGCGAGAGCAAGGTGATGATC 5397

QY 4626 AGGAGATCTCTGCCCGGCACTTCCGCCAATAGCAGCAAGTCCCTTCCCGCTTCAGTGACA 4685  
Db 5398 AGGAGATCTCTGCCCGGCACTTCCGCCAATAGCAGCAAGTCCCTTCCCGCTTCAGTGACA 5457  
QY 4686 AGGTGAGCAGAGCTGCGCAAGGAAAGCGCGTGTGTGAGCGACAGATGAGCGCGTGC 4745  
Db 5458 AGGTGAGCAGAGCTGCGCAAGGAAAGCGCGTGTGTGAGCGACAGATGAGCGCGTGC 5517  
QY 4746 TGTCTGCAAGTTCAATTCAGGCGACCGGACAGGTGCTTGAACAAAAAACCAGCGCGC 4805  
Db 5518 TGTCTGCAAGTTCAATTCAGGCGACCGGACAGGTGCTTGAACAAAAAACCAGCGCGC 5577  
QY 4806 CCTGCGTGAAGACCGGCAACAGCGGATCAGAGCAACGATATGCTGTGTGCGCAG 4865  
Db 5578 CCTGCGTGAAGACCGGCAACAGCGGATCAGAGCAACGATATGCTGTGTGCGCAG 5637  
QY 4866 TCATAGCCGAAATAGCTCTCCACCCAGCGCGCGAGAACTGCGTCAATCATCTTGT 4925  
Db 5638 TCATAGCCGAAATAGCTCTCCACCCAGCGCGCGAGAACTGCGTCAATCATCTTGT 5697  
QY 4926 TCATCATGCGAAACGATCTCATCTGTCTTGTATCATGATCTTGTATCCCTGCGCAT 4985  
Db 5698 TCATCATGCGAAACGATCTCATCTGTCTTGTATCATGATCTTGTATCCCTGCGCAT 5757  
QY 4986 CAG 4988  
Db 5758 CAG 5760

RESULT 12  
AAV33629/C  
ID AAV33629 standard; DNA; 5594 BP.  
XX  
XX AAV33629;  
XX  
XX 29-DEC-1998 (first entry)  
XX  
DE GENSA 981, a monomeric DNA sequence produced by the invention.  
XX  
XX  
XX Class IIS restriction endonuclease recognition site;  
XX endogenous mouse promoter element; tissue-specific gene expression;  
XX hormone-specific gene expression; ss;  
XX developmental-specific gene expression.  
XX  
OS Synthetic.  
XX  
XX WO9838326-A1.  
XX  
XX 03-SEP-1998.  
XX  
XX 28-FEB-1998; 98WO-US003918.  
XX  
XX 28-FEB-1997; 97US-0070910P.  
XX  
XX (NATU-) NATURE TECHNOLOGY CORP.  
XX  
XX Hodgson CP, Zink MA, Xu G;  
XX  
XX WPI; 1998-495399/42.  
XX  
XX  
XX Method for assembling gene or gene vector - comprises use of primers  
XX containing class IIS restriction endonuclease recognition sites.  
XX  
XX Example 2; Page 107-110; 141bp; English.  
XX  
XX The invention provides a novel method for directing self-assembly of a  
XX gene having three or more fragments in a directionally and spatially  
XX ordered fashion to produce a gene or a gene vector. The method involves  
XX usage of primers, containing class IIS restriction endonuclease  
XX recognition sites, for isolation of these fragments. As described in the  
XX disclosure, the method may also use a vector for the incorporation and  
XX screening of endogenous mouse promoter elements for the identification of

CC cell specific promoters. In the example given, plasmids pBK-CMV  
CC (AAV33626), pVLAMB (AAV33623) and pVIOVGH-900 (AAV33621) were used as  
CC templates from which six fragments were amplified. Each of the fragments  
CC contained different regulatory sequences. The six PCR fragments were  
CC designed to self-assemble into a retro-vector using the method of the  
CC invention. The present sequence, designated as GENS 981, represents the  
CC monomeric DNA sequence of the six ligated fragments. In general, the  
CC method is claimed to be useful for isolating and identifying regulatory  
CC sequences from a cell, including those for enhanced biological activity,  
CC or tissue-specific, hormone-specific or developmental-specific gene  
CC expression  
CC  
XX  
SQ

Sequence 5594 BP; 1232 A; 1519 C; 1518 G; 1325 T; 0 U; 0 Other;

Query Match 31.3%; Score 1652.4; DB 2; Length 5594;

Best Local Similarity 85.4%; Pred. No. 116-241;

Matches 1916; Conservative 0; Mismatches 261; Indels 67; Gaps 4;

QY 3107 CCGGGTTGCTGGCGCTTTTTCATAGGCTCCGCCCCCTGACGAGCATCAAAAATCGAC 3166  
DB 5591 CCGGGTTGCTGGCGCTTTTTCATAGGCTCCGCCCCCTGACGAGCATCAAAAATCGAC 5532  
QY 3167 GCTCAAGTCAAGAGTGGCGAAACCCGACAGACTATAAGATACAGGCGTTTCCCTCG 3226  
DB 5531 GCTCAAGTCAAGAGTGGCGAAACCCGACAGACTATAAGATACAGGCGTTTCCCTCG 5472  
QY 3227 GAAGCTCCCTGGTGGCTCTCTGTTCGACCCCTGACCCGATACCTGTCCTGCT 3286  
DB 5471 GAAGCTCCCTGGTGGCTCTCTGTTCGACCCCTGACCCGATACCTGTCCTGCT 5412  
QY 3287 TTCTCCCTTCCGGAAGCGTGGCGCTTTTCTCATAGCTGAGTATCTCAGTTCCG 3346  
DB 5411 TTCTCCCTTCCGGAAGCGTGGCGCTTTTCTCATAGCTGAGTATCTCAGTTCCG 5352  
QY 3347 TGTAGTGTGCTGCTCCAGCTGGCTGTGTGCAAGAACCCCGCTTCCGCGCCT 3406  
DB 5351 TGTAGTGTGCTGCTCCAGCTGGCTGTGTGCAAGAACCCCGCTTCCGCGCCT 5292  
QY 3407 GCGGCTTATCCGGTAACTATGCTGTGATGCAACCCGGTAAAGACAGACTTATCGCAC 3466  
DB 5291 GCGGCTTATCCGGTAACTATGCTGTGATGCAACCCGGTAAAGACAGACTTATCGCAC 5232  
QY 3467 TGGGAGAGCCACTGTGTAAAGATTAAGCAGAGGAGTATGTAGCGGCTCTACAGAT 3526  
DB 5231 TGGGAGAGCCACTGTGTAAAGATTAAGCAGAGGAGTATGTAGCGGCTCTACAGAT 5172  
QY 3527 TCTTGAAGTGTGCTTAACTAAGCTGCTAAGAAAGAGTATTTGGTATCTGCGCTC 3586  
DB 5171 TCTTGAAGTGTGCTTAACTAAGCTGCTAAGAAAGAGTATTTGGTATCTGCGCTC 5112  
QY 3587 TGTGGAAGCCAGTTAACTTCCGAAAAAGATTTGTGATCTTGAATCCGGCAAAACCA 3646  
DB 5111 TGTGGAAGCCAGTTAACTTCCGAAAAAGATTTGTGATCTTGAATCCGGCAAAACCA 5052  
QY 3647 CCGGCTGTAGCGGTGTTTGTGTTTTCAGCAGCAGATTAACGGCGAGAAAAAGAT 3706  
DB 5051 CCGGCTGTAGCGGTGTTTGTGTTTTCAGCAGCAGATTAACGGCGAGAAAAAGAT 4992  
QY 3707 CTCAAGAAAGATCTTGAATCTTTTCTAAGGGGTCTGACGCTC-----AGTGAACG 3757  
DB 4991 GGTGTGGGCTCTTTTATTTAGAGCTCGGGGACAGAAAGCGCGAAACGAGAAAGCG 4932  
QY 3758 AAAAAGCTTAAGGATTTTGTGATGATATATGTCGACCAAGAGCGGCTATGTCG 3817  
DB 4931 AACTGATTTGTTAGTTCAAAATTAAGGACAGGGTCTTTCAGAGTCTTTGGGGCAACCTGGA 4872  
QY 3818 CTC-----CCCACTCTGACAGTTGCGGGGCGATGATGCGGCGATACCGCTG 3864  
DB 4871 AACAATGTAGATGTTCTGTAGAAACTGTGAGGGCTGACCGCATCTGGGAGACATCTGTT 4812  
QY 3865 CTGCTTTCTGTAGATGCGACGAGATTTGC-----ACTGCGGTGAGAACTCCGCGAG 3914  
DB 4811 CTGGCCCTGAGCGGGGACAGAACTGCTTACACAGATATCTGTTGGCCATATTTCA 4752

QY 3915 GTCCGACGCTTCAGGACGAGCTGAACCACTGCGGAGGGGATCGAGCCCGGGGTGGC 3974  
DB 4751 GCTGTTTCATCTGTTCTTGGCTTGAAGCGGGGACGAGACTGCTTACCAAGATCTCTG 4692  
QY 3975 GAAGAATCCAGCATGAGATCCCGCGTGAAGATCAATCCAGCGCGGTCCGAAAAAC 4034  
DB 4691 TTGGGCCATATTCAGCTGTTCCATCTGCTCTGACCTGTATGAACTTCTATCTTC 4632  
QY 4035 GATTCCGAAGCCCACTTTATGAAAGCGCGGTGAATCGAAATTCG----- 4085  
DB 4631 AGTTATGATTTTTCATGCTTCGCAAAATGCGCTTACTTAAGCTATTCGCAAACTTA 4572  
QY 4086 -----TGATGACAGATTTGGGCGTGGCTTGGCTGCTAT 4119  
DB 4571 CAGTGGGCTTTTTCATTTCCCTTTTCTGAGGTTTGGCGTGGCTTGGCTGCTAT 4512  
QY 4120 TCGAACCAGAGTCCCGCTCAGAAAGACTCTGTCAGAAAGCGATAGAAAGCGATGCGCT 4179  
DB 4511 TCGAACCAGAGTCCCGCTCAGAAAGACTCTGTCAGAAAGCGATAGAAAGCGATGCGCT 4452  
QY 4180 GCGAATGGGAGCGGCGATACCTTAAGACAGAGAAAGCGGTACGCCATTCGCGCAA 4239  
DB 4451 GCGAATGGGAGCGGCGATACCTTAAGACAGAGAAAGCGGTACGCCATTCGCGCAA 4392  
QY 4240 GCTCTGAGCAATATCACGGGTACCAAGCGTATGCTCTGATAGCGGTCCGCGCAACCA 4299  
DB 4391 GCTCTGAGCAATATCACGGGTACCAAGCGTATGCTCTGATAGCGGTCCGCGCAACCA 4332  
QY 4300 GCCCGCACAGTGCATGATATCAAGAAAGCGGCAATTTCCACATGATATTTCCGCAAGC 4359  
DB 4331 GCCCGCACAGTGCATGATATCAAGAAAGCGGCAATTTCCACATGATATTTCCGCAAGC 4272  
QY 4360 AAGCATGCCATGGGTGTCAGACGATCTCTGCGGTGGGATGCGGCGCTTGAAGCTGG 4419  
DB 4271 AAGCATGCCATGGGTGTCAGACGATCTCTGCGGTGGGATGCGGCGCTTGAAGCTGG 4212  
QY 4420 CGAAGCTGGGCTGGGCGAGGCCCTGATGCTTTGCTCAGATCAATCCGATCGACAA 4479  
DB 4211 CGAAGCTGGGCTGGGCGAGGCCCTGATGCTTTGCTCAGATCAATCCGATCGACAA 4152  
QY 4480 GACCGGCTTCATCCAGTACGTGCTGCTGATGCGATGTTTGGTGTGATGCAATG 4539  
DB 4151 GACCGGCTTCATCCAGTACGTGCTGCTGATGCGATGTTTGGTGTGATGCAATG 4092  
QY 4540 GGCAGTACCGGATCAAGGCTATGACGCGCGCATTTGATCAATGCAATGATGATCTT 4599  
DB 4091 GGCAGTACCGGATCAAGGCTATGACGCGCGCATTTGATCAATGCAATGATGATCTT 4032  
QY 4600 TTTCCGAGAGAGCAAGGTGATGACAGAGATCTTCCCGGACCTTCCGCAATGCA 4659  
DB 4031 TTTCCGAGAGAGCAAGGTGATGACAGAGATCTTCCCGGACCTTCCGCAATGCA 3972  
QY 4660 GCGAGTCCCTTCCGCTTCAAGTACAGAGTCAAGCAGCTGCGCAAGAAAGCGCGTGC 4719  
DB 3971 GCGAGTCCCTTCCGCTTCAAGTACAGAGTCAAGCAGCTGCGCAAGAAAGCGCGTGC 3912  
QY 4720 TGGCAGCCACGATAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4779  
DB 3911 TGGCAGCCACGATAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3852  
QY 4780 CCGTCTTGAAGAAAGAAACCGGGGCGCGCGCGCTGCAACCGGAAACCGGGCGATCAG 4839  
DB 3851 CCGTCTTGAAGAAAGAAACCGGGGCGCGCGCGCTGCAACCGGAAACCGGGCGATCAG 3792  
QY 4840 AGCAGCCGATTTGTTGTGCGCAGTCAATAGCGAATAGCTCTCACCAAGCGCGCG 4899  
DB 3791 AGCAGCCGATTTGTTGTGCGCAGTCAATAGCGAATAGCTCTCACCAAGCGCGCG 3732  
QY 4900 GAGAACCTGCGTGCATTCATCTTTTCAATGAGAAAGATCTCTCATCTGCTCTT 4959  
DB 3731 GAGAACCTGCGTGCATTCATCTTTTCAATGAGAAAGATCTCTCATCTGCTCTT 3672

QY 4960 GATCAGATCTTATGCCCTGCGCATCAGATCTTGGCGGCAAGAAAGCCATCCAGTTTA 5019  
| | | | |  
Db 3671 GATCAGATCTTATGCCCTGCGCATCAGATCTTGGCGGCAAGAAAGCCATCCAGTTTA 3612  
| | | | |  
QY 5020 CTTTGGCAGGGGCTTCCCAACCTTACAGAGGGGCGCCAGCGTGGCAATTCGGTTCCGTTG 5079  
| | | | |  
Db 3611 CTTTGGCAGGGGCTTCCCAACCTTACAGAGGGGCGCCAGCGTGGCAATTCGGTTCCGTTG 3552  
| | | | |  
QY 5080 CTGTGCATTAACACCGCCAGTCTAGTATCGCATGTATAGCCCACTGCAAGTACCTGCT 5139  
| | | | |  
Db 3551 CTGTGCATTAACACCGCCAGTCTAGTATCGCATGTATAGCCCACTGCAAGTACCTGCT 3492  
| | | | |  
QY 5140 TTTCTTTTGGCGCTTGGCTTTTCCCTTGTCCAGATAGCCCACTGCAATTCATCCGGG 5199  
| | | | |  
Db 3491 TTTCTTTTGGCGCTTGGCGCTTTTCCCTTGTCCAGATAGCCCACTGCAATTCATCCGGG 3432  
| | | | |  
QY 5200 GTACAGACCCGTTTGTGGGAGATGAGCTTTTACGTTCCGCTTCTTTAGACGCCCTTGC 5259  
| | | | |  
Db 3431 GTACAGACCCGTTTGTGGGAGATGAGCTTTTACGTTCCGCTTCTTTAGACGCCCTTGC 3372  
| | | | |  
QY 5260 GCCCTGAGTGCTTGCAGGAGCGGTG 5283  
| | | | |  
Db 3371 GCCCTGAGTGCTTGCAGGAGCGGTG 3348  
| | | | |

RESULT 13  
AEA43088/C  
ID AEA43088 standard; DNA; 4189 BP.  
XX  
AC AEA43088;  
XX  
AC  
XX  
DT 25-AUG-2005 (first entry)  
XX  
DE M. smegmatis perhydrolase expression vector pMSATncoll.  
XX  
KW perhydrolase; bleaching; paper; pulp; cosmetics; vector; ds.  
XX  
OS Mycobacterium smegmatis.  
XX  
OS Synthetic.  
XX  
PN WO2005056782-A2.  
XX  
PD 23-JUN-2005.  
XX  
PF 03-DEC-2004; 2004WO-US040438.  
XX  
PR 03-DEC-2003; 2003US-0526764P.  
XX  
PA (GEMV ) GENENCOR INT INC.  
XX  
PA (PROC ) PROCTER & GAMBLE CO.  
XX  
PI Amin NS, Boston MG, Bott RR, Cervin MA, Concar EM, Guetwiller MB,  
PI Jones BE, Liebeton K, Miracle GS, Oh H, Poulrose AJ, Ramer SW,  
PI Scheibel JJ, Weyler W, Whited GW;  
XX  
DR WPI; 2005-458588/46.  
XX  
PT New isolated perhydrolase having preset perhydrolase to hydrolysis  
PT ratio, useful in cleaning, bleaching and disinfecting applications e.g.  
PT paper pulp bleaching.  
XX  
PS Example 4; SEQ ID NO 13; 523pp; English.  
XX  
CC The invention relates to an isolated perhydrolase (I), exhibiting a  
CC perhydrolase to hydrolysis ratio that is greater than 1. A composition  
CC containing (I) is useful for cleaning. (I) is useful in cleaning,  
CC bleaching and disinfecting applications such as paper and pulp bleaching,  
CC fabric and garment cleaning, hard surface cleaning and personal care  
CC applications (e.g. oral care, hair care, and skin care). (I) is useful in  
CC applications where peracid hydrolysis is useful, such as in the clean up  
CC of peracids. (I) enables effective cleaning, bleaching and disinfecting  
CC over broad pH and temperature ranges. The present sequence represents a  
CC M. smegmatis perhydrolase expression vector.

XX  
SQ Sequence 4189 BP; 895 A; 1168 C; 1217 G; 909 T; 0 U; 0 Other;  
Query Match 30.9%; Score 1634.4; DB 14; Length 4189;  
Best Local Similarity 80.6%; Pred. No. 6.3e-239;  
Matches 2082; Conservative 0; Mismatches 211; Indels 291; Gaps 3;  
QY 2942 CTTCCGCTTCCCTGCTCACTGACCTGCGTCCGCTGCTTCCGCTGCGGAGCGGAT 3001  
| | | | |  
Db 4189 CTTCCGCTTCCCTGCTCACTGACCTGCGTCCGCTGCTTCCGCTGCGGAGCGGAT 4130  
| | | | |  
QY 3002 CAGCTCACTCAAAAGCGGTATACCGTTATCCACAGAAATCAGGGATTAACGAGGAAAGA 3061  
| | | | |  
Db 4129 CAGCTCACTCAAAAGCGGTATACCGTTATCCACAGAAATCAGGGATTAACGAGGAAAGA 4070  
| | | | |  
QY 3062 ACATGTAGCAAAAGCGGCAAGAAAGCCAGAACCGTTAAAGGCCGCTGCTGGGCT 3121  
| | | | |  
Db 4069 ACATGTAGCAAAAGCGGCAAGAAAGCCAGAACCGTTAAAGGCCGCTGCTGGGCT 4010  
| | | | |  
QY 3122 TTTTCCATAGGCTCCGCCCCCTGACAGACATCAAAAATGAGGCTCAAGTCAGAGGT 3181  
| | | | |  
Db 4009 TTTTCCATAGGCTCCGCCCCCTGACAGACATCAAAAATGAGGCTCAAGTCAGAGGT 3950  
| | | | |  
QY 3182 GCGGAAACCCGACAGGACTATTAAGATACAGGCGTTTCCCTGGAAGCTTCCGTGTC 3241  
| | | | |  
Db 3949 GCGGAAACCCGACAGGACTATTAAGATACAGGCGTTTCCCTGGAAGCTTCCGTGTC 3890  
| | | | |  
QY 3242 GCTCTCTGTTCCGACCCCTGCTTACCGGATATCTGTCGCGCTTCTCCCTTGGGGA 3301  
| | | | |  
Db 3889 GCTCTCTGTTCCGACCCCTGCTTACCGGATATCTGTCGCGCTTCTCCCTTGGGGA 3830  
| | | | |  
QY 3302 GCGTGGCGCTTCTCTATAGCTACGCTGAGGATCTCAGTTCCGCTGATGCTTTCGCT 3361  
| | | | |  
Db 3829 GCGTGGCGCTTCTCTATAGCTACGCTGAGGATCTCAGTTCCGCTGATGCTTTCGCT 3770  
| | | | |  
QY 3362 CCAAGCTGGGCTGTGTGACAGAACCCCGTTCAAGCCGACCGCTGCTTATCCGTA 3421  
| | | | |  
Db 3769 CCAAGCTGGGCTGTGTGACAGAACCCCGTTCAAGCCGACCGCTGCTTATCCGTA 3710  
| | | | |  
QY 3422 ACTATGCTCTTGAAGTCAACCCGGTAAAGCAGACTTATCCGCACTGGAGAGGACACTG 3481  
| | | | |  
Db 3709 ACTATGCTCTTGAAGTCAACCCGGTAAAGCAGACTTATCCGCACTGGAGAGGACACTG 3650  
| | | | |  
QY 3482 GTAAAGAGATTAGCAGAGGAGGATATGAGCGGCTCTACAGATTCTTGAAGTGAGC 3541  
| | | | |  
Db 3649 GTAAAGAGATTAGCAGAGGAGGATATGAGCGGCTCTACAGATTCTTGAAGTGAGC 3590  
| | | | |  
QY 3542 CTAACTACGGCTTACCTAGAAAGACGTAATTTGTATCTGCGCTGCTGAAGCCAGTTA 3601  
| | | | |  
Db 3589 CTAACTACGGCTTACCTAGAAAGACGTAATTTGTATCTGCGCTGCTGAAGCCAGTTA 3530  
| | | | |  
QY 3602 CCTTCGAAAAAAGATTGTAAGTCTTGAATCCGCGAAACAAACCCGCTGATGAGCGGTG 3661  
| | | | |  
Db 3529 CCTTCGAAAAAAGATTGTAAGTCTTGAATCCGCGAAACAAACCCGCTGATGAGCGGTG 3470  
| | | | |  
QY 3662 GTTTTGTGTTGCAAGCAGAGATTAACCGCAGAAAAAAGAGATCTCAAGAGATCTT 3721  
| | | | |  
Db 3469 GTTTTGTGTTGCAAGCAGAGATTAACCGCAGAAAAAAGAGATCTCAAGAGATCTT 3410  
| | | | |  
QY 3722 TGAATCTTTCTACAGGAGTCTGACGCTCAGTGAAGAAACCTCAGTTAAGGATTTTGG 3781  
| | | | |  
Db 3409 TGAATCTTTCTACAGGAGTCTGACGCTCAGTGAAGAAACCTCAGTTAAGGATTTTGG 3350  
| | | | |  
QY 3782 TCATGAGATTATC----- 3794  
| | | | |  
Db 3349 TCATGAGATTATCAAAAAGAGATCTTCACTTCTTTTAATTAATAATGAAGTTTA 3290  
| | | | |  
QY 3795 -----GTGACCA 3802  
| | | | |  
Db 3289 GCAAGTGTACGTCTGCTCTCTGCGCAAGATGACGAGTTGCCGCGCGGTCCGCA 3230  
| | | | |  
QY 3803 AAGCGGCATCGTGCCTCCCACTCTCTGCAAGTTCCGCGGCAATGATGCCGATACCCG 3862  
| | | | |

Dh 3229 GGGCGAATCCCGCCCGCCGAGCTGCTCGCGATCTGAGTGGCGCGCGCGCGAGGCGT 31170  
Qy 3863 TGTGTGTTTCTGTGATGCGGACGAGATTGCACTGCGGTAAGAACTCCGCGAGTGTCTCA 3922  
Dh 3169 CCCGGAATGTGTGACACGACCTCCGACCACTCGGCGTACAGCTCTGTCAGGCGCGCA 3110  
Qy 3923 GCC----- 3925  
Dh 3109 CCCACACCCAGGCGCAGGTTGTGTCGCGACCACTGCTCTGACCGCGCTGATGACA 3050  
Qy 3926 ---TCAGGACAGCTGTAACCACTCGGAGAGGATTCAGCCCGGAGTGGCGAAGAACT 3982  
Dh 3049 GGGTACGCTGTCCCGGACCAACCGGAGTGTCTCTCAAGAAATCCCGGAGAAC 2990  
Qy 3983 CCAGCATAGATATCCCGGCTGAGAGATCATCCAGCGCGCGTCCCGGAAAAGATTCGGA 4042  
Dh 2989 CGAGCCGCTCGGTCCAGAACTCGACCGCTCCGCGACACTCGCGCGGTGAGCACCGGA 2930  
Qy 4043 AGCCCAACCTTTCATAGAAAGCGCGGTGAATCGAAATCTGATGCGAGTGGGCG 4102  
Dh 2929 CGGACATGTCATCTTGGCAGTGGTGGCCCTCTCAAGTGTATTTGAAGCAATTAATC 2870  
Qy 4103 TCGCTGTGTCGATTTTCGAAACCCAGATCCG----- 4137  
Dh 2869 AGGGTTATTGTCTCATAGAGCGAATCATATTGAAATGATTTAGAAAATAACAAATAG 2810  
Qy 4138 ----- 4137  
Dh 2809 GGGTTCGGCGCACTTTCGCCGAAAAGTCCCACTGTATGCGGTGTGAATATCCGACAG 2750  
Qy 4138 -----CTCAGAAATTC 4150  
Dh 2749 ATGCGTAAGGAAATATACGCGATCAGGAATTTGTAAGCTTAAATTCAGAAATTC 2690  
Qy 4151 GTCAGAAAGCGATAGAAAGCGATGCGTGCAGATTCGGAGCGCGGATACCGTAAGCAC 4210  
Dh 2689 GTCAAGAAAGCGATAGAAAGCGATGCGTGCAGATTCGGAGCGCGGATACCGTAAGCAC 2630  
Qy 4211 GAGGAGCGGTCAAGCCATTCGCGCGCAAGCTTTTCAGCAATATCACGGGTATGCGCAACGC 4270  
Dh 2629 GAGGAGCGGTCAAGCCATTCGCGCGCAAGCTTTTCAGCAATATCACGGGTATGCGCAACGC 2570  
Qy 4271 TATGCTGATAGCGGTTCGCGCACACCGCGCGCACAGTGCATGATCCAGAAAGCG 4330  
Dh 2569 TATGCTGATAGCGGTTCGCGCACACCGCGCGCACAGTGCATGATCCAGAAAGCG 2510  
Qy 4331 GCCATTTTCCACATGATATTTGCGCAAGCAGCATTCGCGATGGTCAAGCAGATCTC 4390  
Dh 2509 GCCATTTTCCACATGATATTTGCGCAAGCAGCATTCGCGATGGTCAAGCAGATCTC 2450  
Qy 4391 GCGGTGCGGAGATGCGCGCTTTGAGCTGCGGAAACAGTTGCGTGGCGGAGCCCTGATG 4450  
Dh 2449 GCGGTGCGGAGATGCGCGCTTTGAGCTGCGGAAACAGTTGCGTGGCGGAGCCCTGATG 2390  
Qy 4451 CTCCTTCAGATCATCTGATGACAGACCGGCTTTCATTCGAGTACGTCGCTC 4510  
Dh 2389 CTCCTTCAGATCATCTGATGACAGACCGGCTTTCATTCGAGTACGTCGCTC 2330  
Qy 4511 GATGCGATGTTTGTGTTGTGATGAGCAGTACCGGATCAAGCGTATGCAACCG 4570  
Dh 2329 GATGCGATGTTTGTGTTGTGATGAGCAGTACCGGATCAAGCGTATGCAACCG 2270  
Qy 4571 CCGCATTCGATTCAGCCATGATGATATCTTCTCGCGAGAGCAAGTGAAGTGAAGAG 4630  
Dh 2269 CCGCATTCGATTCAGCCATGATGATATCTTCTCGCGAGAGCAAGTGAAGTGAAGAG 2210  
Qy 4631 ATCTGCGCGGCACTTCGCGCAATAGACAGCAGTCCCTTCGCGTCAAGTCAAGTGC 4690  
Dh 2209 ATCTGCGCGGCACTTCGCGCAATAGACAGCAGTCCCTTCGCGTCAAGTCAAGTGC 2150  
Qy 4691 GAGCAGAGTTCGCGAGAAACCGCGCTGTGCGCAGCAGCAGTATGCGCGTGTCTGTC 4750  
Dh 2149 GAGCAGAGTTCGCGAGAAACCGCGCTGTGCGCAGCAGCAGTATGCGCGTGTCTGTC 2090

Qy 4751 CTGAGTTTATTTCAGGGCACCGACAGGTGCGTCTTGAACAAAAGAACCGGCGCCCTG 4810  
Dh 2089 TTGCAATTCATTCAGGGCACCGACAGGTGCGTCTTGAACAAAAGAACCGGCGCCCTG 2030  
Qy 4811 CGTGAAGCGCGAACAACCGGCGATCAGACAGCCGATGTTGTGTTGTGCCAGTCA 4870  
Dh 2029 CGTGAAGCGCGAACAACCGGCGATCAGACAGCCGATGTTGTGTTGTGCCAGTCA 1970  
Qy 4871 GCCCAATAGCTCTTCACCCAGGCGCGGAGAACCTGCGTGCATTCATTTGTTCAAT 4930  
Dh 1969 GCCCAATAGCTCTTCACCCAGGCGCGGAGAACCTGCGTGCATTCATTTGTTCAAT 1910  
Qy 4931 CATGCGAAAGCATCTGATCTGCTGTGATGATGATCTTGAATCCCGTGGCGCATTCAGT 4990  
Dh 1909 CATGCGAAAGCATCTGATCTGCTGTGATGATGATCTTGAATCCCGTGGCGCATTCAGT 1850  
Qy 4991 CTTGCGCGCAAGAAACCATTCAGTTTACTTTGACAGGCGTTCCCACTTACAGAGGG 5050  
Dh 1849 CTTGCGCGCGAAGAAACCATTCAGTTTACTTTGACAGGCGTTCCCACTTACAGAGGG 1790  
Qy 5051 CGCCCAAGCTGCGAATTCGCGTTCGCTGCTGTCATPAAAACGCCAGTCTAGCTATCG 5110  
Dh 1789 CGCCCAAGCTGCGAATTCGCGTTCGCTGCTGTCATPAAAACGCCAGTCTAGCTATCG 1730  
Qy 5111 CCATGTAAGCCCACTGCAAGTACTGCTTCTCTTGGCGCTTCCCTTGTCCA 5170  
Dh 1729 CCATGTAAGCCCACTGCAAGTACTGCTTCTCTTGGCGCTTCCCTTGTCCA 1670  
Qy 5171 GATAGCCCAATGCTGATTCATTCGCGGCTGACGACCGTTTCTGCGGACTGCTTCTA 5230  
Dh 1669 GATAGCCCAATGCTGATTCATTCGCGGCTGACGACCGTTTCTGCGGACTGCTTCTA 1610  
Qy 5231 CGTG 5234  
Dh 1609 CGTG 1606

RESULT 14  
ADU71288/c  
ID ADU71288 standard; DNA; 4245 BP.  
XX  
XX ADU71288;  
AC  
XX 06-MAY-2004 (first entry)  
DT  
XX  
DE PCR-BiuntII-TOPO cloning vector containing M13 primers.  
KW  
XX  
XX de; vector; DNA amplification; sequencing; collapsible emulsion.  
OS  
XX Synthetic.  
PN  
XX WO2003106678-A1.  
XX  
XX 24-DEC-2003.  
PD  
XX  
XX 13-JUN-2003; 2003WO-AU000746.  
PR  
XX 13-JUN-2002; 2002AU-00002981.  
XX  
XX (NUCL-) NUCLEICS PRY LTD.  
PA  
XX  
XX Tillec D, Thomas T;  
PI  
XX  
XX WPI; 2004-191031/18.  
XX  
XX  
PS Disclosure; Fig 1; 11pp; English.  
XX  
XX The present invention relates to a method of performing a chemical  
CC reaction between reactants, which involves subjecting an emulsion  
CC comprising a discontinuous first phase in which at least one of the  
CC reactants is present, and a continuous second phase, to a physical or  
CC chemical change such that a continuous phase is formed from the











Mon May 15 09:36:48 2006

us-09-921-143-36.rng

Page 27

Job time : 1973 secs

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GenCore version 5.1.8  
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OM nucleic - nucleic search, using sw model

Run on: May 13, 2006, 17:56:56 ; Search time 12708 Seconds  
(without alignments)  
19450.437 Million cell updates/sec

Title: US-09-921-143-36  
Perfect score: 5283  
Sequence: 1 aagcttgacctatgcgacgac.....tgagctgctgcgcgcagcgtg 5283

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_hsc:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_est7:\*  
9: gb\_gsa1:\*  
10: gb\_gsa2:\*  
11: gb\_gsa3:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1008.4	19.1	1186	8	DR045845 FP-10_F08
2	1003.6	19.0	1176	8	CX943193 LamGestG
3	991	18.8	2450	4	AK047844 Mus muscu
4	948	17.9	1067	1	AU081137 AU081137
5	939.4	17.8	954	7	CK283361 EST746083
6	924.6	17.5	947	7	CK298208 EST760922
7	919.8	17.4	1089	1	AU081124 AU081124
8	918.6	17.4	935	7	CK284786 EST747508
9	911	17.2	936	7	CK256977 EST740614
10	907	17.2	910	7	CK287930 EST750652
11	897.4	17.0	1049	10	CL021189 CH216-8A1
12	886.4	16.8	933	7	CK291799 EST754513
13	881	16.7	951	8	CY983341 UMC-bot_0
14	875	16.6	925	6	CB686151 Bn01b_02o
15	866.2	16.4	1073	6	CP269652 Fcy1col1d8
16	859.2	16.3	885	10	CL076016 CH216-138
17	856.8	16.2	875	8	CX012952 1o62d12.b
18	854	16.2	1191	8	DR045882 FP-11_A09
19	843	16.0	856	7	CK287297 EST750019
20	826	15.6	868	8	CY984340 UMC-bov_0
21	820.6	15.5	1025	10	CL021193 CH216-8A1
22	820	15.5	894	8	DN641029 UMC-bend_

23	818.6	15.5	833	8	CX013029 1o62h07.b
24	818.6	15.5	1169	10	AG332951 Mus muscu
25	813.8	15.4	1195	8	DR046031 FP-8_F02
26	809.8	15.3	813	8	CX006605 1o23F10.b
27	809.2	15.3	966	9	B2570738 msn2_1513
28	805.8	15.3	865	7	CK125894 BES1B2411
29	803	15.2	804	7	CK291519 EST754233
30	800.4	15.2	804	8	CY979032 UMC-bentiv
31	794	15.0	811	7	CK288185 EST750907
32	792	15.0	808	11	DE103081 Oryzias 1
33	792	15.0	810	11	DE097025 Oryzias 1
34	792	15.0	810	11	DE097277 Oryzias 1
35	792	15.0	810	11	DE097360 Oryzias 1
36	792	15.0	810	11	DE097448 Oryzias 1
37	792	15.0	810	11	DE097511 Oryzias 1
38	792	15.0	810	11	DE098632 Oryzias 1
39	792	15.0	810	11	DE099849 Oryzias 1
40	792	15.0	810	11	DE100113 Oryzias 1
41	792	15.0	810	11	DE102302 Oryzias 1
42	792	15.0	810	11	DE104910 Oryzias 1
43	792	15.0	810	11	DE104989 Oryzias 1
44	792	15.0	833	11	DE096768 Oryzias 1
45	792	15.0	833	11	DE097610 Oryzias 1

## ALIGNMENTS

RESULT 1  
LOCUS DR045845 1186 bp mRNA linear EST 02-JUN-2005  
DEFINITION FP-10\_F08.SFO cDNA library of Phaeosphaeria nodorum grown on wheat cell walls Phaeosphaeria nodorum cDNA, mRNA sequence.

ACCESSION DR045845  
VERSION DR045845.1 GI:66909681  
KEYWORDS EST.  
SOURCE Phaeosphaeria nodorum  
ORGANISM Phaeosphaeria nodorum

REFERENCE Eukaryotes; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;  
Pleosporeales; Phaeosphaeriaceae; Phaeosphaeria.  
1 (bases 1 to 1186)  
Bindschedler,L.V., Cooper,R.M., Thomas,S.W., Madrid,M.P. and Oliver,R.P.

TITLE cDNA library of Phaeosphaeria nodorum grown on wheat cell walls  
JOURNAL Unpublished (2005)  
CONTACT: Richard Oliver  
AUSTRALIAN CENTRE FOR NECROTROPHIC FUNGAL PATHOGENS (ACNFP)  
MURDOCH UNIVERSITY  
SOUTH STREET, MURDOCH, W.A 6150, AUSTRALIA  
Tel: +0893607404  
Email: roliver@murdoch.edu.au.

FEATURES  
source Location/Qualifiers  
1..1186  
/organism="Phaeosphaeria nodorum"  
/mol\_type="mRNA"  
/db\_xref="taxon:13684"  
/clone\_lib="cDNA library of Phaeosphaeria nodorum grown on wheat cell walls"

## ORIGIN

Query Match 19.1%; Score 1008.4; DB 8; Length 1186;  
Best local similarity 99.2%; Pred. No. 1.2e-278; Indels 2; Gaps 2;  
Matches 1034; Conservative 0; Mismatches 6;  
QY 2711 CGTATCATGTCATAGCTGTTCTGTTGTAATTGTTATCCGCTCAATTCACACA 2770  
DB 23 CGTATCATGTCATAGCTGTTCTGTTGTAATTGTTATCCGCTCAATTCACACA 82  
QY 2771 ACATACAGCCGGAAGCATTAAGTAAAGCTGGGGTGGCTAATAGTACGTAATCA 2830  
DB 83 ACATACAGCCGGAAGCATTAAGTAAAGCTGGGGTGGCTAATAGTACGTAATCA 142  
QY 2831 CATTATTCGTTGCGCTCACTGCCGCTTTCAGTGCAGGAACCTGTCGACGCTGC 2890

Db	143	CATTAAATGGGTGGCTCACTGCGGCTTTCCAGTGGGAAACTGTGTCGCACTG	202
OY	2891	ATTATGAATGCGCCACAGCGCGGGAGAGCGGTTTGCATATGGCGCTCTTCGCTT	2950
Db	203	ATTATGATATGGCCAAACGCGCGGGAGAGCGGTTTGGCATTTGGGCGCTTTCGCTT	262
OY	2951	CTCGCTCACTGACTCGCTGCGCTGCGTCTGTTGCGGCTGCGCGCAGCGGTATTCAGCTCACT	3010
Db	263	CTCGCTCACTGACTCGCTGCGCTGCGTCTGTTGCGGCTGCGCGCAGCGGTATTCAGCTCACT	322
OY	3011	CAAAAGCGGTATTCGGTTATCCACATATCAGGGAGTAAACGACGAGAAACATGTGAG	3070
Db	323	CAAAAGCGGTATTCGGTTATCCACATATCAGGGAGTAAACGACGAGAAACATGTGAG	382
OY	3071	CAAAAGCGCAGCAAAAGGCGCAGAAACCGTAAANAGCCGCGTTGCTGGCGTTTTCCATA	3130
Db	383	CAAAAGCGCAGCAAAAGGCGCAGAAACCGTAAANAGCCGCGTTGCTGGCGTTTTCCATA	442
OY	3131	GGCTTCGCGCCCCCTGACGAGATATCAAAAAATGACGCTCAAGTCAAGGTGGCAAAAC	3190
Db	443	GGCTTCGCGCCCCCTGACGAGATATCAAAAAATGACGCTCAAGTCAAGGTGGCAAAAC	502
OY	3191	CGACGAGACTATAAAGATACCAGGCGTTTCCCGCTGAAAGCTCCCTCGTGCCTCTCTG	3250
Db	503	CGACGAGACTATAAAGATACCAGGCGTTTCCCGCTGAAAGCTCCCTCGTGCCTCTCTG	562
OY	3251	TTTCGACCCCTGCGCTTACCGGATTCCTGTCCGCTTCTCCCTTCGGAAAGCGTGGCGC	3310
Db	563	TTTCGACCCCTGCGCTTACCGGATTCCTGTCCGCTTCTCCCTTCGGAAAGCGTGGCGC	622
OY	3311	TTTCTCATAGCTCAAGCTGTAGTATCTCAGTTCCGATAGTGGTTCGCTCCAAAGCTGG	3370
Db	623	TTTCTCATAGCTCAAGCTGTAGTATCTCAGTTCCGATAGTGGTTCGCTCCAAAGCTGG	682
OY	3371	GCTGTGTGCAAGAACCCGCCGTTACGCCGACCGCTGCGCTTATCCGGTAACTATGTGC	3430
Db	683	GCTGTGTGCAAGAACCCGCCGTTACGCCGACCGCTGCGCTTATCCGGTAACTATGTGC	742
OY	3431	TTTGAATCCAAACCCGGTAAACACCATTTATGCCATCTGGACGACGCCATGTATACAGGA	3490
Db	743	TTTGAATCCAAACCCGGTAAACACCATTTATGCCATCTGGACGACGCCATGTATACAGGA	802
OY	3491	TTAGCAGAGCGAGTATGATGAGCGGTGCTCAAGATTTTGAAGTGTGGCTTAACG	3550
Db	803	TTAGCAGAGCGAGTATGATGAGCGGTGCTCAAGATTTTGAAGTGTGGCTTAACG	862
OY	3551	GCTACACTAGANAGAACGATATTTGATATCTGCGCTCTGCTGAGCACTTACCTTCGGAA	3610
Db	863	GCTACACTAGANAGAACGATATTTGATATCTGCGCTCTGCTGAGCACTTACCTTCGGAA	922
OY	3611	AAAGAGTTGGTATGCTCTTGAATCCGGCAACAAACACGCGGTATGCGGTGGTATTTT	3670
Db	923	AAAGAGTTGGTATGCTCTTGAATCCGGCAACAAACACGCGGTATGCGGTGGTATTTT	982
OY	3671	TTTGCAAGCAGCAGATTACGCGCAGAAAAAAGATCTCAAGAGATCTTTGATCTTTT	3730
Db	983	TTTGCAAGCAGCAGATTACGCGCAGAAAAAAGATCTCAAGAGATCTTTGATCTTTT	1040
OY	3731	CTACGGGGTCTGACGCTCACTG	3752
Db	1041	CTACGGGGTCTGACGCTCACTG	1062

RESULT 2					
CX943193					
LOCUS		1176 bp	mRNA	linear	EST 09-FEB-2005
DEFINITION	CX943193				
	IamjesesGS8 Laminaria japonica Iambda Zap Express Library Laminaria				
ACCESSION	CX943193				
VERSION	CX943193.1				
KEYWORDS	GI:58802440				
SOURCE	EST:				
	Laminaria japonica				

ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Laminaria japonica	1	Xuan, J., Zhao, G., Wang, W., Duan, D., Weng, M. and Wang, B.	Expressed sequence tag analysis of the brown alga Laminaria japonica (Phaeophyceae)	Unpublished (2005)	
Bukariyora: stramenopiles; Phaeophyceae; Laminariales; Laminariaceae; Laminaria.	1 (bases 1 to 1176)				
Science	Datum Road, Chaoyang District, Beijing, China, 100101				
Institute of Genetics and Developmental Biology, Chinese Academy of	Tel: 086 010 64889353				
	Fax: 086 010 64873428				
	Email: bhuixuan@hotmail.com				
	Seq primer: T3 Forward				
	High quality sequence stop: 1176.				
Location/Qualifiers	1. 1176				
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/mol_type="mRNA"					
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/sex="female"					
/dev_stage="gametophyte"					
/clone_lib="Laminaria japonica Lambda Zap Express Library"					
/note="Vector: Uni-ZAP® XR vector; Site_1: EcoRI; Site_2: XhoI"					
ORIGIN					
Query Match	19.0%;	Score 1003.6;	DB 8;	Length 1176;	
Best Local Similarity	98.4%;	Pred. No. 2.e-277;	Indels 8;	Gaps 5;	
Matches 1067;	Conservative 0;	Mismatches 9;			
Db	2711	CGTATCATGCTCTAGCTGTTTCTGTGAAATTGTATTCGCGTCACAAATTCACACA	2770		
QY	37	CGTATCATGCTCTAGCTGTTTCTGTGAAATTGTATTCGCGTCACAAATTCACACA	96		
Db	2771	ACATACGAGCGGAGGACATTAAGTGTAAAGCTTGGGCTGCTTAATGATGATCA	2830		
QY	97	ACATACGAGCGGAGGACATTAAGTGTAAAGCTTGGGCTGCTTAATGATGATCA	156		
Db	2831	CATTATTCGCTGCGCTACTGCGCGCTTCCAGTGGGAAACCTTCGTCAGCTGC	2890		
QY	157	CATTATTCGCTGCGCTACTGCGCGCTTCCAGTGGGAAACCTTCGTCAGCTGC	216		
Db	2891	ATTATGATGATGGCGCAACGCGCGGGAGAGCGGTTTGCGTATTTGGGCGCTTCCGCTT	2950		
QY	217	ATTATGATGATGGCGCAACGCGCGGGAGAGCGGTTTGCGTATTTGGGCGCTTCCGCTT	276		
Db	2951	CCTGCTCACTGACTCGCTGCGCTCGGCTTCGCTTCGCGCTTCGCGCGAGCGGTACACT	3010		
QY	277	CCTGCTCACTGACTCGCTGCGCTCGGCTTCGCTTCGCGCTTCGCGCGAGCGGTACACT	336		
Db	3011	CAAAAGCGGTATACGGTTATCCACAGATCAGGGGATTAAGCGAGAAAGATGTGAG	3070		
QY	337	CAAAAGCGGTATACGGTTATCCACAGATCAGGGGATTAAGCGAGAAAGATGTGAG	396		
Db	3071	CAAAAGCGCGACAAAGGCGCAGAAACGCTAATAAGCCGCGTTCGCGCTTTTCCATA	3120		
QY	397	CAAAAGCGCGACAAAGGCGCAGAAACGCTAATAAGCCGCGTTCGCGCTTTTCCATA	456		
Db	3131	GGCTCCGCCCCCTTACGACGATCACAATAATCAGCGTCAAGTCAGAGGTGGGAAAC	3190		
QY	457	GGCTCCGCCCCCTTACGACGATCACAATAATCAGCGTCAAGTCAGAGGTGGGAAAC	516		
Db	3191	CGACGAGACTATTAAGATACGAGCGTTTCCCTCGAAGCTCCCTCGTCGCTCTCTG	3256		
QY	517	CGACGAGACTATTAAGATACGAGCGTTTCCCTCGAAGCTCCCTCGTCGCTCTCTG	576		
Db	3251	TTTCGACCCCTGCGCTTACCGGATACCTGTCGCTTCTCTGCTTCGGGAAGCGTGGGC	3310		
QY	577	TTTCGACCCCTGCGCTTACCGGATACCTGTCGCTTCTCTGCTTCGGGAAGCGTGGGC	636		

OY		3311	TTTTCATPAGCCTCAGCGGTAGTAATCTCAGTTCCGGTAGAGTGCTGTGCCTCCAAAGCTGG	337
Db		637	TTTTCATTACTACAGCGCTAGATATCTAAGTTCCGGTAGAGTGCTGTGCCTCCAAAGCTGG	696
OY		3371	GCTGTGTGACGAACCCCCCGTTACGCCGCCAGCCGCTCATTCGGATACTATCGTC	3433
Db		697	GCTGTGTGACGAACCCCCCGTTACGCCGCCAGCCGCTCATTCGGATACTATCGTC	756
OY		3431	TTCGATCCCAACCCGGTAAACAACAATTATCGCCACTGCGACAGACCCTAGTAAACAGA	3499
Db		757	TTGAGTTCCAACCCGGTAAACAACAATTATCGCCACTGCGACAGACCCTAGTAAACAGA	816
OY		3491	TTAGCAGACGCAAGTATGTAGAGCGGTGCTACAGAGTCTTGAAAGTGAGGCGCTACTACG	3555
Db		817	TTAGCAGACGCAAGTATGTAGAGCGGTGCTACAGAGTCTTGAAAGTGAGGCGCTACTACG	876
OY		3551	GCTACACTAGAAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACTTCGGAA	3610
Db		877	GCTACACTAGAAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACTTCGGAA	936
OY		3611	AAAAGTTGTGTAGCTCTTGATTCGGCAAACAACACCGCTGTGTATGCGGTGTTTTTTG	3670
Db		937	AAAAGTTGTGTAGCTCTTGATTCGGCAAACAACACCGCTGTGTATGCGGTGTTTTTTG	995
OY		3671	TTTGCAGACGACGAGTTACGGCGCACAAAAAAAAGATCTCAAGAAATCCTTTGATCTTTT	3730
Db		996	TTTGCAGACGACGAGTTACGGCGCACAAAAAAA--GGATCTCAAGAAATCCTTTGATCTTTT	10533
OY		3731	CTACGGGGCTTGACCGCTCAGTGAAGCAAAAACTCAGCTTAAAGGATTTTGTCTAGAGAT	3790
Db		1054	CTAC-GGGTCTGACGCTCAGTG--ACGAACTCAGCTT-AGGATTTTGTCTAGAGAT	1108
OY		3791	TATC	3794
Db		1109	TATC	1112
<hr/>				
RESULT 3				
AK047844				
LOCUS				
DEFINITION		AK047844	2450 bp mRNA linear HTC 03-APR-2004	
		Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched		
		library, clone:C130004M09 product:vascular endothelial growth		
		factor C, full insert sequence.		
ACCESSION		AK047844		
VERSION		AK047844.1 GI:26339001		
KEYWORDS		HTC; CAP trapper.		
SOURCE		Mus musculus (house mouse)		
ORGANISM		Mus musculus		
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
		Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;		
		Sciuromorphi; Muridae; Murinae; Mus.		
REFERENCE				
AUTHORS		Carninci,P. and Hayashizaki,Y.		
TITLE		High-efficiency full-length cDNA cloning		
JOURNAL		Meth. Enzymol. 303, 19-44 (1999)		
PUBMED		10349636		
REFERENCE				
AUTHORS		Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,		
		Itoh,M., Komno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.		
TITLE		Normalization and subtraction of cap-trapper-selected cDNAs to		
JOURNAL		prepare full-length cDNA libraries for rapid discovery of new genes		
PUBMED		Genome Res. 10 (10), 1617-1630 (2000)		
REFERENCE		11042159		
AUTHORS				
		Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,		
		Komno,H., Akiyama,U., Nishi,K., Kitsuma,T., Tashiro,H., Itoh,M.,		
		Sunai,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,		
		Yamanoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,		
		Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Matsubiki,M.,		
		Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuzaki,S., Kawal,U.,		
		Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and Hayashizaki,Y.		
		RIKEN integrated sequence analysis (RISA) system--384-format		
TITLE				

REFERENCE	JOURNAL	PUBMED	GENOME RES.	SCORE	DB	LENGTH	CDNA
11076861	Genome Res.	10 (11), 1757-1771	(2000)	18.8%	Score 991;	DB 4;	Length 2450;
4	The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.			85.4%;	Pred. No. 1.6e-273;		
5	Nature	409, 685-690	(2001)				
6	(bases 1 to 2450)						
7	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanakawa, T., Katoh, H., Kawai, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohnato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.						
8	Submitted (16-Jun-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suenho-cho, Tsurumi-ku, Yokohama Kanagawa 230-0045, Japan (E-mail: genome-res@gs.c.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)						
9	CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.						
10	Please visit our web site for further details.						
11	URL: http://genome.gsc.riken.jp/						
12	URL: http://fantom.gsc.riken.jp/						
13	Location/Qualifiers						
14	1. 2450						
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19	/db_xref="taxon:10090"						
20	/clone="C130004M09"						
21	/tissue_type="head"						
22	/clone_lib="RIKEN full-length enriched mouse cDNA library"						
23	/dev_stage="16 days embryo"						
24	175. 1422						
25	/note="unamed protein product; putative vascular endothelial growth factor C (MGD GI:109124, GI NM_009506, evidence: BLASTN, 99%, match=1784)"						
26	/codon_start=1						
27	/protein_id="BAC33172.1"						
28	/db_xref="GI:26339002"						
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Db	262	GCTGATTATGATATGGCCAAACGGCGGGGAGAGCGGCTTTGCGTATTGGGGCTTTC	321
OY	2946	CGCTTCTTCGCTCACTGACTCGTCGCGCTCGGTCTTCGCTGCGGCGAGCGGTATCAGC	3005
Db	322	CGCTTCTCGCTCACTGACTCGCGTGCGCTCGGTCTTCGCTGCGGCGAGCGGTATCAGC	381
OY	3006	TCACTCAAAAGCGGTAATCGGTTATCCACAGATCAGGGGATTAACGACGAGAAAGACAT	3065
Db	382	TCACTCAAAAGCGGTAATCGGTTATCCACAGATCAGGGGATTAACGACGAGAAAGACAT	441
OY	3066	GTAGCAAAAAGGCGAGCAAAAAGGCGAGAACCGGTAAAAAGGCGCGGTTCGCGCTTTT	3125
Db	442	GTAGCAAAAAGGCGAGCAAAAAGGCGAGAACCGGTAAAAAGGCGCGGTTCGCGCTTTT	501
OY	3126	CCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCG	3185
Db	502	CCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCG	561
OY	3186	AAACCCGACAGGACTATTAAGATACGAGCGTTTCCTCCCTGGAAGCTCCTCGTCGCTC	3245
Db	562	AAACCCGACAGGACTATTAAGATACGAGCGTTTCCTCCCTGGAAGCTCCTCGTCGCTC	621
OY	3246	TCCTGTTCCGACCCCTGCGCTTACCGGATACCTGTCCGCTTTCCTTCCTTCGGGAAAGGT	3305
Db	622	TCCTGTTCCGACCCCTGCGCTTACCGGATACCTGTCCGCTTTCCTTCCTTCGGGAAAGGT	681
OY	3306	GGCGCTTCTCACTAGCTCAAGCTGTAGGATCTCAGTTCGAGTTCGAGTTCGTTCCGCTCA	3365
Db	682	GGCGCTTCTCACTAGCTCAAGCTGTAGGATCTCAGTTCGAGTTCGAGTTCGTTCCGCTCA	741
OY	3366	GCTGGGCTGTGTGCAAGAACCCCGCTTCAAGCCGACGCGTGGCGCTTATCCGTAACTA	3425
Db	742	GCTGGGCTGTGTGCAAGAACCCCGCTTCAAGCCGACGCGTGGCGCTTATCCGTAACTA	801
OY	3426	TCGTCTTAGATCCAAACCCGCTTAAGACACGACTTATTCGCCACTGGCAGACGCCACTGGTAA	3485
Db	802	TCGTCTTAGATCCAAACCCGCTTAAGACACGACTTATTCGCCACTGGCAGACGCCACTGGTAA	861
OY	3486	CAGATTGACAGAGGAGGATATGTAGGGGGGTCTACAGTTCCTGAAGTGTGGCCCTAA	3545
Db	862	CAGATTGACAGAGGAGGATATGTAGGGGGGTCTACAGTTCCTGAAGTGTGGCCCTAA	921
OY	3546	CTACGGCTACACTAGAAAGACAGTATTTGTATCTGCGCTCTGCTGAAGCCAGTTACCTT	3605
Db	922	CTACGGCTACACTAGAAAGACAGTATTTGTATCTGCGCTCTGCTGAAGCCAGTTACCTT	981
OY	3606	CGAAAAAAGAGTGGTAGCTTTGATCCGGCAAAACAAACAACCGCTGTAGCGGTGTTT	3665
Db	982	CGAAAAAAGAGTGGTAGCTTTGATCCGGCAAAACAAACAACCGCTGTAGCGGTGTTT	1040
OY	3666	TTTTGTTTGCACGACGAGATTACGGCGC 3693	
Db	1041	TTTTGTTTGC-AGCAGCAGATTACGGCGC 1067	

RESULT	5
LOCUS	CK283361/c
DEFINITION	CK283361 954 bp mRNA linear EST 02-AUG-2004 EST7746083 Nicotiana benthamiana mixed tissue cDNA library, normalized, full-length Nicotiana benthamiana cDNA clone NBWAG50 5'
ACCESSION	CK283361
VERSION	CK283361.1 GI:39855698
KEYWORDS	EST.
SOURCE	Nicotiana benthamiana
ORGANISM	Nicotiana benthamiana
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamiales; Solanales; Solanaceae; Nicotiana. 1 (bases 1 to 954)
AUTHORS	Buell,C.R., Hart,A., Zisman,V., Karamycheva,S.A., Day,B., Stebkavicz,B., Jin,H. and Baker,B.

TITLE		Generation of EST sequences from <i>Nicotiana benthamiana</i>	
JOURNAL		Unpublished (2003)	
COMMENT		Other_ESTs: EST746094	
		Contact: Robin Buell	
		The Institute for Genomic Research	
		9712 Medical Center Dr. Rockville, MD 20850, USA	
		Email: potato-array@igr.org	
		Clones can be requested from the University of Arizona Genomics	
		Institute via <a href="http://genome.arizona.edu/orders/">http://genome.arizona.edu/orders/</a> .	
		Seq primer: ATT TAG GTG ACA CTA TAG.	
FEATURES		Location/Qualifiers	
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		callus tissue and root tissue"	
		/lab_host="DHI0B-Tona"	
		/clone_id="Nicotiana benthamiana mixed tissue cDNA	
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		/note="Vector: pCMVSPORT6.1; Site.1: EcoRI; Site.2: NotI;	
		supplier: RNA was isolated from Nicotiana benthamiana	
		tissues that include callus, roots from liquid culture	
		grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),	
		cold-stressed leaves (5 C 3 hr, 6hr), and pathogen	
		challenged leaves (Pseudomonas syringae pv tomato 12 hr;	
		Xanthomonas campestris pv campestris 12 hr, 18hr;	
		Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas	
		campestris pv vesicatoria 18hr). RNA was isolated from	
		these tissues and pooled in approximately equal molar	
		amounts."	
ORIGIN			
Query Match 17.8%; Score 939.4; DB: 7; Length 954;			
Best Local Similarity 99.9%; Pred. No. 8.9e-259;			
Matches 940; Conservative 1; Mismatches 1; Indels 0; Gaps 0;			
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Y	3991 AGATCCCCGCGCTGGAGGATCATCACCCGGCGTCCGGAAAAAGATTCGAGAGCCCAAC	4050	
Db	954 AGATCCCCGCGCTGGAGGATCATCACCCGGCGTCCGGAAAAAGATTCGAGAGCCCAAC	895	
Y	4051 CTTTCATGAAAGCGCGGTGGAAATCGAAATCTTGTGATGAGCAGTTGGCGCTGGCTTG	4110	
Db	894 CTTTCATGAAAGCGCGGTGGAAATCGAAATCTTGTGATGAGCAGTTGGCGCTGGCTTG	835	
Y	4111 TCGGTCAATTCGAAACCCCAAGATCCCGCTCAAGAAACTGCTCAAGAAAGCGATGAAAG	4170	
Db	834 TCGGTCAATTCGAAACCCCAAGATCCCGCTCAAGAAACTGCTCAAGAAAGCGATGAAAG	775	
Y	4171 CGATGCGCTGGGAATCGGAGCGCGCGATACCGTAAACAAGAGAGCGGTCAAGCCATT	4230	
Db	774 CGATGCGCTGGGAATCGGAGCGCGCGATACCGTAAACAAGAGAGCGGTCAAGCCATT	715	
Y	4231 CGCGCGCAAGCTTTGACGAATATCAAGGGTAGCCACGCTATGTCGTGATAGGGCTCCG	4290	
Db	714 CGCGCGCAAGCTTTGACGAATATCAAGGGTAGCCACGCTATGTCGTGATAGGGCTCCG	655	
Y	4291 CCACACCCAGCGCGCCACAGTCGATGATTCAGAAAAAGCGCAATTTTCCACATGATAT	4350	
Db	654 CCACACCCAGCGCGCCACAGTCGATGATTCAGAAAAAGCGCGCAATTTTCCACATGATAT	595	
Y	4351 TCGGCAAGCAAGGATCGGCATGGGTCAAGACGAGATCTTGCGCTGGGGATAGGGCGCT	4410	
Db	594 TCGGCAAGCAAGGATCGGCATGGGTCAAGACGAGATCTTGCGCTGGGGATAGGGCGCT	535	
Y	4411 TGAAGCTGGGAAACAGTTTCGGCTGGCGCGAGCCCTGATGCTCTTTCGTCCAGATCATCT	4470	
Db	534 TGAAGCTGGGAAACAGTTTCGGCTGGCGCGAGCCCTGATGCTCTTTCGTCCAGATCATCT	475	
Y	4471 GATCGACAAAGACGGGCTTCATCCGAGATCGTGTGCTTCGATGCGATGTTTGGCTTGGT	4530	
Db	474 GATCGACAAAGACGGGCTTCATCCGAGATCGTGTGCTTCGATGCGATGTTTGGCTTGGT	415	

QY 4531 GGTCGAATGGGACAGTAGCCGGATCAACGGTATGACACCGCCGATTCATGACCACTGA 4530  
Db 414 GGTGAATGGGACAGTAGCCGGATCAACGGTATGACACCGCCGATTCATGACCACTGA 355  
QY 4591 TGAATACCTTCTCGGACAGGACAGTAGATGACAGAGATCTCGCCCGGACCTTCG 4650  
Db 354 TGAATACCTTCTCGGACAGGACAGTAGATGACAGAGATCTCGCCCGGACCTTCG 295  
QY 4651 CCAATACAGACCAATCCCTTCCGCTTCAGTGAACAGTGCAGACAGCTGCAGAGAA 4710  
Db 294 CCAATACAGACCAATCCCTTCCGCTTCAGTGAACAGTGCAGACAGCTGCAGAGAA 235  
QY 4711 CGCCCGCTGAGCAGCAGATAGCCGCTGCTGCTGAGTTCATTCAGGCGAC 4770  
Db 234 CGCCCGCTGAGCAGCAGATAGCCGCTGCTGCTGAGTTCATTCAGGCGAC 175  
QY 4771 CGGACAGGTGCTTGTGACAAAAAGAACCGGGCGCCCTGCGTGAACGCGGAACAG 4830  
Db 174 CGGACAGGTGCTTGTGACAAAAAGAACCGGGCGCCCTGCGTGAACGCGGAACAG 115  
QY 4831 CGGACAGGTGCTTGTGACAAAAAGAACCGGGCGCCCTGCGTGAACGCGGAACAG 4890  
Db 114 CGGACAGGTGCTTGTGACAAAAAGAACCGGGCGCCCTGCGTGAACGCGGAACAG 55  
QY 4891 AAGCGCGGAGAACCTGCGTCAATCATCTTGTCAATC 4931  
Db 54 AAGCGCGGAGAACCTGCGTCAATCATCTTGTCAATC 14

RESULT 6  
CK298208/c 947 bp mRNA linear EST 02-AUG-2004  
LOCUS EST760922 Nicotiana benthamiana mixed tissue cDNA library, NBMDE30 5'  
DEFINITION normalized, full-length Nicotiana benthamiana cDNA clone NBMDE30 5'  
end, mRNA sequence.  
CK298208  
CK298208.1 GI:39885354  
EST.  
SOURCE Nicotiana benthamiana  
ORGANISM Nicotiana benthamiana  
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
asterids; lamiales; Solanales; Solanaceae; Nicotiana.  
1 (bases 1 to 947)  
Buell, C.R., Hart, A., Zismann, V., Karanicheva, S.A., Day, B.,  
Stackawicz, B., Jin, H. and Baker, B.  
Generation of EST sequences from Nicotiana benthamiana  
unpublished (2003)  
Other ESTs: EST760923  
Contact: Robin Buell  
The Institute for Genomic Research  
9712 Medical Center Dr, Rockville, MD 20850, USA  
Email: potato-array@tigr.org  
Clones can be requested from the University of Arizona Genomics  
Institute via <http://genome.arizona.edu/orders/>.  
Seq primer: ATT TAG GTG ACA CTA TAG.  
Location/Qualifiers  
1..947  
/organism="Nicotiana benthamiana"  
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/db\_xref="taxon:4100"  
/clone="NBMDE30"  
/tissue\_type="abiotic and biotic stress-treated leaves,  
callus tissue and root tissue"  
/lab\_host="PH10B-Tona"  
/clone\_lib="Nicotiana benthamiana mixed tissue cDNA  
library, normalized, full-length"  
/note="Vector: pCMWSPORT6.1; Site 1: EcoRI; Site 2: NotI;  
supplier: RNA was isolated from Nicotiana benthamiana  
tissues that include callus, roots from liquid culture  
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),  
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen

challenged leaves (Pseudomonas syringae pv tomato 12 hr;  
Xanthomonas campestris pv campestris 12 hr, 18hr;  
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas  
campestris pv vesicatoria 18hr). RNA was isolated from  
these tissues and pooled in approximately equal molar  
amounts."

Query Match 17.5%; Score 924.6; DB 7; Length 947;  
Best local similarity 99.6%; Pred. No. 1.7e-254;  
Matches 927; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 4001 GCTGAGGATCATCCAGCCGCGCTCCCGGAAAAAGATTCGGAAGCCCACTTCAATGA 4060  
Db 947 GCTGAGGATCATCCAGCCGCGCTCCCGGAAAAAGATTCGGAAGCCCACTTCAATGA 888  
QY 4061 AGCGCGCGGTGAATGAATCTCGTGAATGAGCAGTGTGGGCGTGGCTGATTCATTT 4120  
Db 887 AGCGCGCGGTGAATGAATCTCGTGAATGAGCAGTGTGGGCGTGGCTGATTCATTT 828  
QY 4121 CGAATCCCAAGTCCCGCTCAGAAAGACTGTCAGAAAGCGATAGAGCGATGCGCTG 4180  
Db 827 CGAATCCCAAGTCCCGCTCAGAAAGACTGTCAGAAAGCGATAGAGCGATGCGCTG 768  
QY 4181 CGAATGCGGAGCGGATACCGCTAAGCAAGAAAGCGGTACGCCATTCGCGCGAAG 4240  
Db 767 CGAATGCGGAGCGGATACCGCTAAGCAAGAAAGCGGTACGCCATTCGCGCGAAG 708  
QY 4241 CTCTTCAGCAATATACCGGGTAGCCCAAGCTATGCTGATAGCGGTCCGCAACCCAG 4300  
Db 707 CTCTTCAGCAATATACCGGGTAGCCCAAGCTATGCTGATAGCGGTCCGCAACCCAG 648  
QY 4301 CCGGCGCAAGTGAATGAATCCGAAAGAGCGCATTTTCACCATGATATTTGGCAGCA 4360  
Db 647 CCGGCGCAAGTGAATGAATCCGAAAGAGCGCATTTTCACCATGATATTTGGCAGCA 588  
QY 4361 GGCATGCGCATGAGTCAAGCAGAGATCTCGCGCGGCGCATGCGGCTTGAAGCTGGC 4420  
Db 587 GGCATGCGCATGAGTCAAGCAGAGATCTCGCGCGGCGCATGCGGCTTGAAGCTGGC 528  
QY 4421 GAAACGTTGGGCTGGCGCAGAGCCCTGATGCTCTTCGTCAGATCATCTGATCGCAAG 4480  
Db 527 GAAACGTTGGGCTGGCGCAGAGCCCTGATGCTCTTCGTCAGATCATCTGATCGCAAG 468  
QY 4481 ACCGGCTTCATCCGAGTACGTCGCTCGCTCAATGCGATGCTTGGCTGGTCCGATGG 4540  
Db 467 ACCGGCTTCATCCGAGTACGTCGCTCGCTCAATGCGATGCTTGGCTGGTCCGATGG 408  
QY 4541 GCAGGTAGCCGATCAAGCGTATGACGCGCGCATTCGATGACGATGATGATCTT 4600  
Db 407 GCAGGTAGCCGATCAAGCGTATGACGCGCGCATTCGATGACGATGATGATCTT 348  
QY 4601 CTCGCGAGGACAGGTGATGACAGAGATCTGCCCCGCACTTCCCAATAGCAG 4660  
Db 347 CTCGCGAGGACAGGTGATGACAGAGATCTGCCCCGCACTTCCCAATAGCAG 288  
QY 4661 CCAAGTCCCTCCCGCTTCAAGTGAACAAGTGAACAAGTGAACAAGTGAACAAGTGA 4720  
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QY 4721 GGCACGACAGATAGCCGCGCTGCTGCTGCTGATTCATTCAGGCGACGCGAGGTC 4780  
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QY 4781 GGTCTTGAACAAAAAGAACCGGCGCGCTTGGCTGACAGCGCGGAAACAGCGCGCATCAGA 4840  
Db 167 GGTCTTGAACAAAAAGAACCGGCGCGCTTGGCTGACAGCGCGGAAACAGCGCGCATCAGA 108  
QY 4841 GAGCGGATGCTGCTGTCGCGCGAGTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 4900  
Db 107 GAGCGGATGCTGCTGTCGCGCGAGTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 48  
QY 4901 AGAACCTGCTGCAATCCATCTTGTCAATC 4931

|||||  
Db 47 AGAACCTGCGTGCATCCATCTTGTTCATC 17  
RESULT 7  
AU081124 1089 bp mRNA linear EST 30-JUL-2002  
LOCUS AU081124 Oncorhynchus mykiss Kidney infected by infectious  
DEFINITION hematopoietic necrosis virus Oncorhynchus mykiss CDNA clone KG.12,  
mRNA sequence.  
ACCESSION AU081124  
VERSION AU081124.1 GI:6431472  
KEYWORDS EST.  
SOURCE Oncorhynchus mykiss (rainbow trout)  
ORGANISM Oncorhynchus mykiss  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
Proclanchopneustei; Salmoniformes; Salmonidae; Oncorhynchus.  
REFERENCE 1 (bases 1 to 1089)  
AUTHORS Kono,T., Sakai,M. and Lapetra,S.E.  
TITLE Expressed Sequence Tag Analysis of Kidney and Gill Tissues from  
Rainbow Trout (Oncorhynchus mykiss) Infected with Infectious  
Hematopoietic Necrosis Virus  
JOURNAL Mar. Biotechnol. 2 (5), 493-498 (2001)  
COMMENT Contact: Masahiro Sakai  
Faculty of Agriculture  
Miyazaki University  
1-1-nishi gakuenkibanadai, Miyazaki, Miyazaki 889-2192, Japan  
Email: m.sakai@cc.miyazaki-u.ac.jp.  
Location/Qualifiers  
FEATURES  
source  
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/organism="Oncorhynchus mykiss"  
/mol\_type="mRNA"  
/db\_xref="taxon:8022"  
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infectious hematopoietic necrosis virus"  
/note="common name:rainbow trout ; infected by infectious  
hematopoietic necrosis virus"  
ORIGIN  
Query Match 17.4%; Score 919.8; DB 1; Length 1089;  
Best Local Similarity 97.2%; Pred. No. 4.2e-253;  
Matches 979; Conservative 0; Mismatches 22; Indels 6; Gaps 4;  
QY 2706 CTGACGCTATCATGTCATGCTGTTCTCTGTGTAATTTGTTATCCGCTCACAATTTCC 2765  
DB 83 CTTGGCCTAATCATGTCATGCTGTTCTCTGTGTAATTTGTTATCCGCTCACAATTTCC 142  
QY 2766 ACACAATCGAGCGGAGCAATTAAGTCTTAAGCCCTGGGGTCCCTAATAGAGAGCTA 2825  
DB 143 ACACAAATACGAGCCGAGACATTAAGTGAAGCCCTGGGGTCCCTAATAGAGAGCTA 202  
QY 2826 ACTCACATTAATTCGTTGGCTCATGCGCTTTCCAGTCGGGAAACCTGTGTGCCA 2885  
DB 203 ACTCAGATTAAATTCGTTGGCTCATGCGCTTTCCAGTCGGGAAACCTGTGTGCCA 262  
QY 2886 GCTGCATTAATGAATCGGCCAACCGCGGGAGAGCGGTTTGGTATTTGGCGCTCTTC 2945  
DB 263 GCTGCATTAATGAATCGGCCAACCGCGGGAGAGCGGTTTGGTATTTGGCGCTCTTC 322  
QY 2946 CGCTTCCTCGCTCATGCTCGCTGCGCTCGTCTCGCTGCGGAGAGCGGTATTCAGC 3005  
DB 323 CGCTTCCTCGCTCATGCTCGCTGCGCTCGTCTCGTCTCGGCGGAGAGGTATCAGC 382  
QY 3006 TCACTCAAGCGCGTAAATACGGTTATCCACAGATTCAGGGGATTAACGAGGAAAGACAT 3065  
DB 383 TCACTCAAGCGCGTAAATACGGTTATCCACAGATTCAGGGGATTAACGAGGAAAGACAT 442  
QY 3066 GTGAGCAAAAGGCCAGCAAAAGGCCAGAACCGTAAAGGCGCGTTGCTGCGGTTTTT 3125  
DB 443 GTGAGCAAAAGGCCAGCAAAAGGCCAGAACCGTAAAGGCGCGTTGCTGCGGTTTTT 502

QY 3126 CCATAGGCTCGGCCCCCTGACGAGCATCAAAAAATGACGCTCAAGTCAAGAGGTGCG 3185  
DB 503 CCATAGGCTCGGCCCCCTGACGAGCATCAAAAAATGACGCTCAAGTCAAGAGGTGCG 562  
QY 3186 AAACCCGACAGACTATTAAGATACAGGCGCTTTCCCTGGAAGCTCCCTGTCGCTC 3245  
DB 563 AAACCCGACAGACTATTAAGATACAGGCGCTTTCCCTGGAAGCTCCCTGTCGCTC 622  
QY 3246 TCTGTTCCGACCTGCGCTTACCGGATACCTGTCCGCTTTCTCCTTGGGAAGCGT 3305  
DB 623 TCTGTTCCGACCTGCGCTTACCGGATACCTGTCCGCTTTCTCCTTGGGAAGCGT 682  
QY 3306 GAGCGTTTCTATAGCTCAGCGTGAAGTATCTAGTTCGGTGAAGTTCGCTCCAA 3365  
DB 683 GAGCGTTTCTATAGCTCAGCGTGAAGTATCTAGTTCGGTGAAGTTCGCTCCAA 742  
QY 3366 GCTGGCGTGTGTGACGAAACCCCGCTTACGACCCGACCGCTGCGCTTATCCGTACTA 3425  
DB 743 GCTGGCGTGTGTGACGAAACCCCGCTTACGACCCGACCGCTGCGCTTATCCGTACTA 802  
QY 3426 TCGTCTTGAAGTCCAAACCGGTAAGACAGACTTATCCGCACTGACAGACGCACTGTAA 3485  
DB 803 TCGTCTTGAAGTCCAAACCGGTAAGACAGACTTATCCGCACTGACAGACGCACTGTAA 862  
QY 3486 CAGATTAGCAGACGAGAGTATGTAAGCGGCTGCTACAGAGTTCTTGAAG--TGTGGCCTA 3544  
DB 863 CAGATTAGCAGACGAGAGTATGTAAGCGGCTGCTACAGAGTTCTTGAAGTTGTGGCCTA 922  
QY 3545 ACTACGCTACACTAGGAAGAACATATTGATCTGCGCTGCTGTAAGCCAGTTACT 3604  
DB 923 ACTACGCTACACTAGGAAGAACATATTGATCTGCGCTGCTGTAAGCCAGTTACT 982  
QY 3605 TCGAAAAAGAGTGTGACTCTT-GATCCGCAAAACA--CCGCTGTGAGCGGT 3660  
DB 983 TCGAAAAAGAGTGTGACTCTTGTGATCCGCAAAACAACCCTGGGAAAGGCGG 1042  
QY 3661 GGTTTTTTTGTTGCAAGCA-GCAGATTACCGCGAGAAAAAAGAT 3706  
DB 1043 TGTCTTTTGTGTGCAAGCAGCAGATTACCCCGAAAAAAGCGAT 1089  
RESULT 8  
CK284786/c 935 bp mRNA linear EST 02-AUG-2004  
LOCUS CK284786  
DEFINITION EST747508 Nicotiana benthamiana mixed tissue cDNA library,  
normalized, full-length Nicotiana benthamiana cDNA clone NBWAQ41.5',  
end, mRNA sequence.  
ACCESSION CK284786  
VERSION CK284786.1 GI:39858639  
KEYWORDS EST.  
SOURCE Nicotiana benthamiana  
ORGANISM Nicotiana benthamiana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
asterids; lamids; Solanales; Solanales; Solanales; Nicotiana.  
REFERENCE 1 (bases 1 to 935)  
AUTHORS Buell,C.R., Hart,A., Zismann,V., Karanymcheva,S.A., Day,B.,  
Skaskawicz,B., Jin,H., and Baker,B.  
TITLE Generation of EST sequences from Nicotiana benthamiana  
JOURNAL Unpublished (2003)  
COMMENT Other\_ESTs: EST747509  
Contact: Robin Buell  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Email: potato-array@tigr.org  
Clones can be requested from the University of Arizona Genomics  
Institute via http://genome.arizona.edu/orders/  
Seq primer: ATT TAG GTG ACA CTA TAG.  
FEATURES  
source  
1..935  
/organism="Nicotiana benthamiana"  
/mol\_type="mRNA"  
Location/Qualifiers

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 /clone\_lib="Nicotiana benthamiana mixed tissue cDNA  
 library, normalized, full-length"  
 /note="Vector: PCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;  
 supplier: RNA was isolated from Nicotiana benthamiana  
 tissues that include callus, roots from liquid culture  
 grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr,  
 cold-stressed leaves (5 C 3 hr, 6hr), and pathogen  
 challenged leaves (Pseudomonas syringae pv tomato 12 hr;  
 Xanthomonas campestris pv campestris 12 hr, 18hr;  
 Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas  
 campestris pv vesicatoria 18hr). RNA was isolated from  
 these tissues and pooled in approximately equal molar  
 amounts."

## ORIGIN

Query Match 17.4%; Score 918.6; DB 7; Length 935;  
 Best Local Similarity 99.6%; Pred. No. 8.9e-253;

Matches 921; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4030 AAAACGATTCGAAACCCCACTTTTCATAGAAAGCGCGGTGGAATGGAATCTCGTAT 4089  
 DB 935 AAAACGATTCGAAACCCCACTTTTCATAGAAAGCGCGGTGGAATGGAATCTCGTAT 876  
 OY 4090 GGCAGGTTGGCGTGGCTGGTGGTCAATTCGAAACCCCAAGTCCCGCTCAGAAAGACT 4149  
 DB 875 GGCAGGTTGGCGTGGCTGGTGGTCAATTCGAAACCCCAAGTCCCGCTCAGAAAGACT 816  
 OY 4150 CGTCAAGAGGCGATAGAAAGCGATGCGCTCGAATGGGAGCGCGCATACCGTAAAGCA 4209  
 DB 815 CGTCAAGAGGCGATAGAAAGCGATGCGCTCGAATGGGAGCGCGCATACCGTAAAGCA 756  
 OY 4210 CGAAGAAAGCGTACGCCCATTCGCGCAAGCTCTTCAGCAATTCACGGGTAGCCAAAG 4269  
 DB 755 CGAAGAAAGCGTACGCCCATTCGCGCAAGCTCTTCAGCAATTCACGGGTAGCCAAAG 696  
 OY 4270 CTATGTCTGATAGCGGTCCGCAACACCCAGCCGCGCAAGTGTGATGATTCAGAAAAAGC 4329  
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 OY 4330 GGCATTTTCCACCATGATATTCGCGCAAGCGGATTCGCGTCAACGAGATCCT 4389  
 DB 635 GGCATTTTCCACCATGATATTCGCGCAAGCGGATTCGCGTCAACGAGATCCT 576  
 OY 4390 GCGCGTGGGCGATGCGCGCTTGAAGCTGCGCAACGATTCGCGTGGCGCGAGCCCTGAT 4449  
 DB 575 GCGCGTGGGCGATGCGCGCTTGAAGCTGCGCAACGATTCGCGTGGCGCGAGCCCTGAT 516  
 OY 4450 GCTTTTCGTCAGATCATCTGATGACAGACCGGCTTCCATCCGATAGCTGTGCT 4509  
 DB 515 GCTTTTCGTCAGATCATCTGATGACAGACCGGCTTCCATCCGATAGCTGTGCT 456  
 OY 4510 CGAATGGAATGTTGCTGGTGGTGGTGAATGGGAGGTAGCCGATCAAGCGTATSCAGC 4569  
 DB 455 CGAATGGAATGTTGCTGGTGGTGGTGAATGGGAGGTAGCCGATCAAGCGTATSCAGC 396  
 OY 4570 GCGCATTTGCATCAGCATGATGATCTTTCTCGGCAAGAGCAAGGTGAGTACAGGA 4629  
 DB 395 GCGCATTTGCATCAGCATGATGATCTTTCTCGGCAAGAGCAAGGTGAGTACAGGA 336  
 OY 4630 GATCTGCCCCCGGCACTTGGCCCAATAGAGCAAGTCCCTTCCAGTGAAGCAAGT 4689  
 DB 335 GATCTGCCCCCGGCACTTGGCCCAATAGAGCAAGTCCCTTCCAGTGAAGCAAGT 276  
 OY 4690 CGAGCAGAGTGGCAAGAAAGCGCGTGTGGCGCAGCAGATAGCGCGCTGCTGCT 4749  
 DB 275 CGAGCAGAGTGGCAAGAAAGCGCGTGTGGCGCAGCAGATAGCGCGCTGCTGCT 216  
 OY 4750 CTTGACGTTTCATTCAAGGAGCAGGACGAGTGGTCTTGAACAAAAGAACCGGCGCCCT 4809

DB 215 CTTGACGTTTCATTCAAGGAGCAGGACAGTGGTCTTGAACAAAAGAACCGGCGCCCT 156  
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 DB 155 GCGTGAACCGCGGAACAACGCGGATCAGAGCAGCGATTTCTGTTGGCCAGTCAT 96  
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 DB 35 TCATGCAAGACGATCCTCATCTGT 11

## RESULT 9

CK256977/c

CK256977 936 bp mRNA linear EST 30-JUL-2004

## LOCUS

DEFINITION EST740614 potato callus cDNA library, normalized and full-length

## ACCESSION

CK256977 Solanum tuberosum cDNA clone PCDD170 5' end, mRNA sequence.

## VERSION

CK256977.1 GI:39813957

## KEYWORDS

EST.

## SOURCE

Solanum tuberosum (potato)

## ORGANISM

Solanum tuberosum

## REFERENCE

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

## AUTHORS

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

## TITLES

asterids; lamids; Solanales; Solanaceae; Solanum.

## JOURNAL

Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.

## COMMENT

Generation of ESTs from potato callus tissue

## JOURNAL

Unpublished (2003)

## CONTACT

Contact: Robin Buell

## INSTITUTE

The Institute for Genomic Research

## ADDRESS

9712 Medical Center Dr, Rockville, MD 20850, USA

## E-MAIL

Email: potato-array@igf.org

## CLONES

Clones can be requested from the University of Arizona Genomics

## INSTITUTE

via http://genome.arizona.edu/orders/

## SEQ PRIMER

Seq primer: ATT TAG GTG ACA CTA TAG.

## FEATURES

Location/Qualifiers

## SOURCE

1..936

## /organism

"Solanum tuberosum"

## /mol\_type

"mRNA"

## /cultivar

"Kennebec"

## /db\_xref

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## /clone

"PCDD170"

## /tissue\_type

"callus"

## /lab\_host

"DH10B-Tona"

## /clone\_lib

"potato callus cDNA library, normalized and

## /note

"Vector: PCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;

## /supplier

RNA was isolated from Solanum tuberosum var.

## /kennebec

callus tissue grown on solid media."

## ORIGIN

Query Match 17.2%; Score 911; DB 7; Length 936;

Best Local Similarity 99.9%; Pred. No. 1.4e-250;

Matches 922; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 4010 TCATCCAGCGGCGTCCC-GGAAGATTCGAAAGCCCAACTTCATAGAAAGCGGCG 4068  
 DB 936 TCATCCAGCGGCGTCCC-GGAAGATTCGAAAGCCCAACTTCATAGAAAGCGGCG 877  
 OY 4069 GTGAATTCGAATCTCGTATGAGCGGCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCT 4128  
 DB 876 GTGAATTCGAATCTCGTATGAGCGGCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCT 817  
 OY 4129 AGAGTCCCGCTCAGAAAGAACTCGTCAAGAAAGGAGGATGAGCGGCTGGAATCGG 4188  
 DB 816 AGAGTCCCGCTCAGAAAGAACTCGTCAAGAAAGGAGGATGAGCGGCTGGAATCGG 757  
 OY 4189 GAGGCGGATACCGTAAAGACAGAGAGCGGTAGCCCATTCGCGCAAGCTTTGAG 4248

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Db      756 GAGCGGCATACCGTAAAGCAGAGAAAGCGGTCAAGCCCATTCGCGCAAGCTCTTCAAG 697
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Db      696 CAATATCAAGGATGACCAACGCTATGCTCTGATAGCGGTCGCGCAACCAAGCGGCGCAC 637
Qy      4309 AGTCGATGAATTCAGAAAAAGCGCCATTTTCCACCATGATATTCGGCAAGAGGCGATCGC 4368
Db      636 AGTCGATGAATTCAGAAAAAGCGCCATTTTCCACCATGATATTCGGCAAGAGGCGATCGC 577
Qy      4369 CATGGGTACCAACGAGATCTTCGCGGTGGGCAATGCGCGCTTGAGCCTTGCGAAACAGTT 4428
Db      576 CATGGGTACCAACGAGATCTTCGCGGTGGGCAATGCGCGCTTGAGCCTTGCGAAACAGTT 517
Qy      4429 CGGCTGGGCGAGCGCCCTGATGCTCTTGTGTCAGATCACTCTGATTCGACAGACCGGCTT 4488
Db      516 CGGCTGGGCGAGCGCCCTGATGCTCTTGTGTCAGATCACTCTGATTCGACAGACCGGCTT 457
Qy      4489 CCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGTTGGTGGTCAATGGGCGAGTAG 4548
Db      456 CCATCCGAGTACGTGCTCGCTCGATGCGATGTTTCGTTGGTGGTCAATGGGCGAGTAG 397
Qy      4549 CCGGATCAAGCGGTATGCAAGCGCGCGCATTTGCATCAAGCCATGATGATATCTTTTCGCGAG 4608
Db      396 CCGGATCAAGCGGTATGCAAGCGCGCGCATTTGCATCAAGCCATGATGATATCTTTTCGCGAG 337
Qy      4609 GAGCAAGGTGATGACAGAGAGATCTTCGCGCGCACTTCGCGCAATGACAGCCAGTCCC 4668
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Qy      4669 TTCCCGCTTCAGTACCAACGTGACAGACAGTGGCGCAAGAGCGCGTCTGGCGAGCC 4728
Db      276 TTCCCGCTTCAGTACCAACGTGACAGACAGTGGCGCAAGAGCGCGTCTGGCGAGCC 217
Qy      4729 ACGATAGCGCGGCTGCTCTGCTGCAAGTTCAATTCAGGGCAACCGCAAGGTCTTTGA 4788
Db      216 ACGATAGCGCGGCTGCTCTGCTGCAAGTTCAATTCAGGGCAACCGCAAGGTCTTTGA 157
Qy      4789 CAAAAAGAACCGGGCGCGCCCTGCGCTGACAGCGCGGAAACAGCGCGGCAATCAAGAGCGCGA 4848
Db      156 CAAAAAGAACCGGGCGCGCCCTGCGCTGACAGCGCGGAAACAGCGCGGCAATCAAGAGCGCGA 97
Qy      4849 TTGCTGTTGTGAGCCAGTCAATAGCCGAATAGCTCTCAACCCAGCGCGCGAGAACCTG 4908
Db      96 TTGCTGTTGTGAGCCAGTCAATAGCCGAATAGCTCTCTCAACCCAGCGCGCGAGAACCTG 37
Qy      4909 CGTGCAATCAATCTTTGTTCAATC 4931
Db      36 CGTGCAATCAATCTTTGTTCAATC 14

RESULT 10
CK287930/c 910 bp mRNA linear EST 02-AUG-2004
LOCUS      EST750652 Nicotiana benthamiana mixed tissue cDNA library,
DEFINITION normalized, full-length Nicotiana benthamiana cDNA clone NMBCT5 5'
            end, mRNA sequence.
ACCESSION  CK287930
VERSION     CK287930.1 GI:39864940
KEYWORDS   EST.
SOURCE      Nicotiana benthamiana
ORGANISM   Nicotiana benthamiana
            Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            asterids; lamiales; Solanales; Solanaceae; Nicotiana.
REFERENCE  1 (bases 1 to 910)
            Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
            Staskiewicz, B., Jin, H. and Baker, B.
            Generation of EST sequences from Nicotiana benthamiana
            Unpublished (2003)
TITLE       Other ESTs: EST750653
COMMENT     Contact: Robin Buell

```

```

FEATURES
source
    The Institute for Genomic Research
    9712 Medical Center Dr, Rockville, MD 20850, USA
    Email: potato-array@igr.org
    Clones can be requested from the University of Arizona Genomics
    Institute via http://genome.arizona.edu/orders/
    Seq primer: ATT TAG GTG ACA CTA TAG.
    Location/Qualifiers
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            /mol_type="mRNA"
            /db_xref="taxon:4100"
            /clone="NMBCT5"
            /c_tissue_type="abiotic and biotic stress-treated leaves,
            callus tissue and root tissue"
            /lab_host="DH10B-TorA"
            /clone_id="Nicotiana benthamiana mixed tissue cDNA
            library, normalized, full-length"
            /note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
            supplier: RNA was isolated from Nicotiana benthamiana
            tissues that include callus, roots from liquid culture,
            grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
            cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
            challenged leaves (Pseudomonas syringae pv tomato 12 hr;
            Xanthomonas campestris pv campestris 12 hr, 18hr;
            Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
            campestris pv vesicatoria 18hr). RNA was isolated from
            these tissues and pooled in approximately equal molar
            amounts."

ORIGIN
Query Match      17.2%; Score 907; DB 7; Length 910;
Best Local Similarity 100.0%; Pred. No. 2e-249;
Matches 907; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4025 CCGGAAAAACGATTCGAGAGCCCAACCTTTCATAGAAAGCGCGGTGAAATCGAAATCTC 4084
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Qy      4085 GTGATGGCAGGTTGGGGGTGGCTTGGTGGTCAATTTGAAACCCCAAGTCCCGTCAAGAA 4144
Db      850 GTGATGGCAGGTTGGGGGTGGCTTGGTGGTCAATTTGAAACCCCAAGTCCCGTCAAGAA 791
Qy      4145 GAACTCGTCAAGAAAGGATAGAAAGGCGATGCGCTGCGAAATCGGGAACCGGATACGCTA 4204
Db      790 GAACTCGTCAAGAAAGGATAGAAAGGCGATGCGCTGCGAAATCGGGAACCGGATACGCTA 731
Qy      4205 AAGCAGAGAGAGCGGTAGAGCCCATTTGCGCGCAAGCTCTTCAGCAATATCACGGGTAGC 4264
Db      730 AAGCAGAGAGAGCGGTAGAGCCCATTTGCGCGCAAGCTCTTCAGCAATATCACGGGTAGC 671
Qy      4265 CAACGCTATGCTCTGATAGCGGTCCGCGACACCAAGCGCGCCACAGTGCATGAATCCAGA 4324
Db      670 CAACGCTATGCTCTGATAGCGGTCCGCGACACCAAGCGCGCCACAGTGCATGAATCCAGA 611
Qy      4325 AAAGCGGCATTTTCCACCATGATATTTGGCAAGAGGCGATTCGCATAGGGTCAAGAGAG 4384
Db      610 AAAGCGGCATTTTCCACCATGATATTTGGCAAGAGGCGATTCGCATAGGGTCAAGAGAG 551
Qy      4385 ATCTCGCGCTCGGGGATGCGCGCTTGAGCCTTGCGGCAAGAGTTTCGCTGCGCGAGCCC 4444
Db      550 ATCTCGCGCTCGGGGATGCGCGCTTGAGCCTTGCGGCAAGAGTTTCGCTGCGCGAGCCC 491
Qy      4445 CTGATGCTCTTGTCCAGATATCTGATGAGCAAGACCGGCTTCCATTCGAGTAGCTGC 4504
Db      490 CTGATGCTCTTGTCCAGATATCTGATGAGCAAGACCGGCTTCCATTCGAGTAGCTGC 431
Qy      4505 TCGCTGATGCGATGTTTGGCTTGTGATGCGATGAGGAGGTAGCGGATCAAGCGTAG 4564
Db      430 TCGCTGATGCGATGTTTGGCTTGTGATGCGATGAGGAGGTAGCGGATCAAGCGTAG 371
Qy      4565 CAGCGCGCGCATTCATCAGCCCATGATGATATCTTTCTCGGCAAGAGCAAGGTGAGATGA 4624
Db      370 CAGCGCGCGCATTCATCAGCCCATGATGATATCTTTCTCGGCAAGAGCAAGGTGAGATGA 311

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QY 4625 CAGAGATCTGCCCCGGGCACTTCCGCAATAGACAGCCAGTCCCTTCCGCTTCAAGTAC 4684  
DB 310 CAGAGATCTGCCCCGGGCACTTCCGCAATAGACAGCCAGTCCCTTCCGCTTCAAGTAC 251  
QY 4685 AAGTGCAGACAGCTGCGGCAAGAAAGCCCGCTGCGGCAAGATGACGCGGCTGC 4744  
DB 250 AAGTGCAGACAGCTGCGGCAAGAAAGCCCGCTGCGGCAAGATGACGCGGCTGC 191  
QY 4745 CTGCTCGTCAAGTTCATTACAGGCGACCGGACAGGTGCTTGAACAAAAGAACCGGCG 4804  
DB 190 CTGCTCGTCAAGTTCATTACAGGCGACCGGACAGGTGCTTGAACAAAAGAACCGGCG 131  
QY 4805 CCCCCTGCTGACACCGGCAACACGCGGCGCATACAGACAGCCGATTTGCTTTGTGCCA 4864  
DB 130 CCCCCTGCTGACACCGGCAACACGCGGCGCATACAGACAGCCGATTTGCTTTGTGCCA 71  
QY 4865 GTCATAGCCGAATAGCTCTTCCACCCGAAGGCGCGGAAAGCTGCGTGAATCATCTTG 4924  
DB 70 GTCATAGCCGAATAGCTCTTCCACCCGAAGGCGCGGAAAGCTGCGTGAATCATCTTG 11  
QY 4925 TTCAATC 4931  
DB 10 TTCAATC 4

RESULT 11  
CL021189 1049 bp DNA linear GSS 31-DEC-2003  
LOCUS CH216-8A14.RM1.1.CH216 Xenopus tropicalis genomic clone CH216-8A14,  
DEFINITION genomic survey sequence.  
ACCESSION CL021189  
VERSION CL021189.1 GI:40463002  
KEYWORDS GSS.  
SOURCE Xenopus tropicalis (western clawed frog)  
ORGANISM Xenopus tropicalis  
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;  
Xenopodinae; Xenopus; Silurana.  
REFERENCE 1 (bases 1 to 1049)  
AUTHORS Kremetzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,  
Mardis,E. and Wilson,R.  
TITLE A physical map of the xenopus tropicalis genome  
JOURNAL Unpublished (2003)  
COMMENT Contact: Richard K Wilson  
Genome Sequencing Center  
Washington University School of Medicine  
Email: submissions@wustl.edu  
Insert Length: 175000 Std Error: 0.00  
Seq primer: RM1.TACGACTCACTATAGGAGAGA  
Class: BAC ends  
High quality sequence start: 43  
High quality sequence stop: 888.  
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/mol\_type="genomic DNA"  
/strain="Nigerian frog"  
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/clone="CH216-8A14"  
/sex="male"  
/cell\_line="Stock 248 F7A2, inbred N7"  
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BAC library"

## ORIGIN

Query Match 17.0%; Score 897.4; DB 10; Length 1049;  
Best Local Similarity 98.1%; Pred. No. 1.2e-246;  
Matches 929; Conservative 0; Mismatches 16; Indels 2; Gaps 2;  
QY 2701 GCTGCTAGACGTAATCATAGTCAATGCTGTTCTCTGTGAATGTATTCGCTCACA 2760  
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DB 102 GCAAGCTTGCGTATCATAGTCAATGCTGTTCTCTGTGAATGTATTCGCTCACA 161  
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DB 162 ATTCAACACATACGAGCGGAAAGCATTAAGTGTAAAGCTGGGGTGCTTAATGAGTG 221  
QY 2821 AGCTAATCAGATTAATGCGTGGCTCACTGCGCCGCTTTCAGTCCGGAAGACCTGTGC 2880  
DB 222 AGCTAATCAGATTAATGCGTGGCTCACTGCGCCGCTTTCAGTCCGGAAGACCTGTGC 281  
QY 2881 TCCAGCTGCAATTAATGAATCGGCAACGCGGGAAGAGCGGTTTGCGTATTGGCGC 2940  
DB 282 TCCAGCTGCAATTAATGAATCGGCAACGCGGGAAGAGCGGTTTGCGTATTGGCGC 341  
QY 2941 TCTTCGCTTCTCTGCTCACTGACTGCTGCGCTGCTGCTTTCGCTGCGGGAACGCTA 3000  
DB 342 TCTTCGCTTCTCTGCTCACTGACTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTA 401  
QY 3001 TCAGCTCACTCAAGCGGTAATACGTTATCAAGATCAGAGATCAGGAGATTAACGAGAAAG 3060  
DB 402 TCAGCTCACTCAAGCGGTAATACGTTATCAAGATCAGGAGATTAACGAGAAAG 461  
QY 3061 AACATGTAGCAAAAAGGCCAGCAAAAGCCGTAAGAGCCGCTTCTGCGC 3120  
DB 462 AACATGTAGCAAAAAGGCCAGCAAAAGCCGTAAGAGCCGCTTCTGCGC 521  
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DB 522 TTTTTCATAGGCTCCGCCCTGACAGCATCAAAAATCGACGCTCAAGTACAGAG 581  
QY 3181 TGGCGAAACCCGACAGCATTAAGATACAGAGGCTTCCCTCGAAGCTCCCTCGTG 3240  
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DB 642 CGCTCTCTGTTCCGACCTGCGCTTACCGGATACCTGTCGCTTTCCTTCGCGGA 701  
QY 3301 AGGTGGGCGCTTTCATAGCTCAAGCTGATGATTCAGTTCGATGAGTGTGCTGCGC 3360  
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QY 3361 TCCAACTGGGCTGTGTGACAGAACCCCGTTCAGCCCGGACCGCTGCGCTTATCCGGT 3420  
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QY 3481 GGTAAAGAGATTAGCAGACGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGTGG 3540  
DB 882 GGTAAAGAGATTAGCAGACGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGTGG 941  
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RESULT 12  
CK291799/c

LOCUS CK291799 933 bp mRNA linear EST 02-AUG-2004  
DEFINITION EST754513 Nicotiana benthamiana mixed tissue cDNA library,  
normalized, full-length Nicotiana benthamiana cDNA clone NBMC477 5'  
end, mRNA sequence.

ACCESSION CK291799.1 GI:39872608  
VERSION CK291799  
KEYWORDS EST.  
SOURCE Nicotiana benthamiana



## ORGANISM

Nicotiana benthamiana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
asterids; lamiales; Solanales; Solanaceae; Nicotiana.

## REFERENCE

1 (bases 1 to 933)  
Buell, C.R., Hart, A., Zismann, V., Karameycheva, S.A., Day, B.,  
Staskiewicz, B., Jin, H. and Baker, B.

## TITLE

Generation of EST sequences from *Nicotiana benthamiana*

## JOURNAL

Unpublished (2003)

## COMMENT

Other ESTs: EST754514

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-array@tigr.org

Clones can be requested from the University of Arizona Genomics

Institute via <http://genome.arizona.edu/orders/>.

## FEATURES

source

Location/Qualifiers

1..933

/organism="Nicotiana benthamiana"

/mol\_type="mRNA"

/db\_xref="taxon:4100"

/clone="NBWC477"

/tissue\_type="abiotic and biotic stress-treated leaves,"

callus tissue and root tissue"

/lab\_host="DH10B-TonA"

/clone\_lib="Nicotiana benthamiana mixed tissue cDNA

library, normalized, full-length"

/note="Vector: pCMVSPORT6.1; Site\_1: EcoRI; Site\_2: NotI;

supplier: RNA was isolated from *Nicotiana benthamiana*

tissues that include callus, roots from liquid culture

grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),

cold-stressed leaves (5 C 3 hr, 6hr), and pathogen

challenged leaves (*Pseudomonas syringae* pv tomato 12 hr;

*Xanthomonas campestris* pv *campestris* 12 hr, 18hr;

*Pseudomonas syringae* pv *phaseolicola* 18hr, and *Xanthomonas*

*campestris* pv *vesicatoria* 18hr). RNA was isolated from

these tissues and pooled in approximately equal molar

amounts."

## ORIGIN

Query Match 16.8%; Score 886.4; DB 7; Length 933;  
Best Local Similarity 99.9%; Pred. No. 1.8e-243;

Matches 887; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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4104 CGCTTGTGCGTCAATTCGAAAGCCCAAGATCCGCTCAGAAAGACTGCTCAAGAAAGCGA 4163

873 CGCTTGTGCGTCAATTCGAAAGCCCAAGATCCGCTCAGAAAGACTGCTCAAGAAAGCGA 814

4164 TAGAAGCGATGCGCTCGATCGGAGCGGCGATACCGTAAACAGAGAAAGCGGTCA 4223

813 TAGAAGCGATGCGCTCGATCGGAGCGGCGATACCGTAAACAGAGAAAGCGGTCA 754

4224 GCCCATTCGCGCGCAAGCTTTCAGCAATATCAGGGTAGCCAAAGCTATGTCTGTATAG 4283

753 GCCCATTCGCGCGCAAGCTTTCAGCAATATCAGGGTAGCCAAAGCTATGTCTGTATAG 694

4284 CGGTCCGCCACACCCAGCGGCGCAAGTCAGTGAATCAGAAAAGCGGCAATTTTCACC 4343

693 CGGTCCGCCACACCCAGCGGCGCAAGTCAGTGAATCAGAAAAGCGGCAATTTTCACC 634

4344 ATGATATTCGGCAAGCAGGATCGCATGGTTCAGCAGAGATCTCGCGTCGGGATG 4403

633 ATGATATTCGGCAAGCAGGATCGCATGGTTCAGCAGAGATCTCGCGTCGGGATG 574

4404 CGGCGCTTGAAGCTCGGGAAGAGTTGGCTGCGCGGAGCCCTGATGCTCTTCCAGA 4463

573 CGGCGCTTGAAGCTCGGGAAGAGTTGGCTGCGCGGAGCCCTGATGCTCTTCCAGA 514

QY 4464 TCATCTGATGACAAAGACCGGCTTCATCCAGATGATGCTGCTCGATGATGTTTC 4523

Db 513 TCATCTGATGACAAAGACCGGCTTCATCCAGATGATGCTGCTCGATGATGTTTC 454

QY 4524 GCTTGTGTGTAATGAGGACAGTATCCGATCAAGCGTATGACCGCGCATTCATCA 4583

Db 453 GCTTGTGTGTAATGAGGACAGTATCCGATCAAGCGTATGACCGCGCATTCATCA 394

QY 4584 GCCATATGATATATTTCTCGCGAGAGCAAGGTGAATGACAGAGATCTTCCCGGCG 4643

Db 393 GCCATATGATATATTTCTCGCGAGAGCAAGGTGAATGACAGAGATCTTCCCGGCG 334

QY 4644 ACTTCGCCAATAGCAGCCAGATCCCTTCGCGCTTCAGTGAACAAGTGAAGAGTGGC 4703

Db 333 ACTTCGCCAATAGCAGCCAGATCCCTTCGCGCTTCAGTGAACAAGTGAAGAGTGGC 274

QY 4704 CAAGAAAGCCCGCTGCTGAGCAGCAAGATAGCCGCTGCTGCTGCTGCTGCTATTC 4763

Db 273 CAAGAAAGCCCGCTGCTGAGCAGCAAGATAGCCGCTGCTGCTGCTGCTGCTATTC 214

QY 4764 AGGCGACCGGACAGGTGCTGTTGACAAAAGAACCGGCGGCGCTGACAGCGCG 4823

Db 213 AGGCGACCGGACAGGTGCTGTTGACAAAAGAACCGGCGGCGCTGACAGCGCG 154

QY 4824 AACACGCGGATCAGACGACCGGATGCTGTTGTCGCAATGACCAATAGGCTC 4883

Db 153 AACACGCGGATCAGACGACCGGATGCTGTTGTCGCAATGACCAATAGGCTC 94

QY 4884 TCACCCCAAGCGGCGGAGAACTGCTGCAATTCATCTTGTTCATTC 4931

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## RESULT 13

CV983341 951 bp mRNA linear EST 30-NOV-2004

LOCUS UMC-boef 0A01-002-g06 Ovarian Follicle boef Bos taurus cDNA 3', mRNA

DEFINITION sequence.

ACCESSION CV983341 GI:56144062

VERSION CV983341.1

KEYWORDS Bos taurus (cow)

SOURCE Bos taurus

ORGANISM Bos taurus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;

Bovidae; Bovinae; Bos.

1 (bases 1 to 951)

Prather, R.S., Antoniou, B., Garverick, H.A., Green, J.A., Lucy, M.C.,

Roberts, R.M., Smith, M.F. and Youngquist, R.S.

USDA Grant NRI-2002-01476; Bovine ESTs: Focus on Female

Reproduction

Unpublished (2002)

Contact: DNA Core Facility (Bovine Project)

Animal Science - RS Prather

University of Missouri-Columbia

1616 Medical Sciences Bldg., Columbia, MO 65212, USA

Tel: (573)882-0428

Fax: (573)884-5552

Email: bovine@rnet.missouri.edu

POLYA=No.

FEATURES

source

Location/Qualifiers

1..951

/organism="Bos taurus"

/mol\_type="mRNA"

/db\_xref="taxon:9913"

/dev\_stage="Ovarian Follicle"

/clone\_lib="bof"

/note="Vector: pSPORT1; Funding: The production of ESTs

submitted in this project was funded by USDA Grant

MRI-2002-01476 entitled 'Bovine ESTs: Focus on Female

Reproduction' to RS Prather (Primary Investigator), B

Antoniou, HA Garverick, JA Green, MC Lucy, RM Roberts, MF

Smith and RS Youngquist. Genetic Source: Heifers for the



project were purchased from Home Circle A Ranch, Iberia, MO (<http://www.circlearanch.com/home.html>). These heifers, while not registered have known Angus pedigrees going back at least 4 generations. Samples collected: The sample consisted of the following: germinal vesicle-stage oocytes; in vitro derived embryos (2-cell), morula, blastocyst and nuclear transfer blastocyst; in vitro blastocysts and conceptuses (days 8, 14, 16 and 18); corpora lutea (days 3, 5, 8, 14, 16, 18 and 35); ovarian follicles (days 0, non-recruited, recruited, early selected and preovulatory); oviduct (days 0, 3 and 5); endometrium (days 5, 8, 14, 16, 18 and 35); and placenta/embryo from day 35 conceptuses. Expanded descriptions of how the tissues were collected can be found at the following URL: <http://genome.mnet.missouri.edu/Bovine/Methods.html>. Library construction (Standard Protocol): All procedures have been described in detail elsewhere (Soares et al., 1994; Bonaldo et al., 1996; Jiang et al., 2001). Total cellular RNA from each sample was isolated by using STAR-60 reagent (Tel-Test, Friendswood, TX) and the poly(A)<sup>+</sup> RNA was obtained by two rounds of purification with the Oligotex mRNA isolation kit (Qiagen) according to the manufacturer's instructions. The libraries were constructed essentially as described by the manufacturer's instructions provided with the Superscript Plasmid System (Invitrogen, cat. no. 18248-013). Briefly, 1mcg of poly(A)<sup>+</sup> RNA was annealed at 37 degrees with 1mcg of NotI-tag-d118 oligonucleotide (GGCTGTCGGCGCGC-tag-T18) and reverse transcribed at 37 degrees with Superscript II (Invitrogen) reverse transcriptase (Jiang et al., 2001). The 'tag' represents a tissue/stage-specific ten-base sequence identifier (<http://genome.uuwa.edu/pubsoft/software.html>) present in the oligonucleotide used to prime first-strand synthesis. Second strand synthesis was performed with T4 DNA polymerase in the presence of DNA ligase and RNase H. After second strand synthesis, the double-stranded cDNAs were ligated to SalI adaptors (Invitrogen-Life Technologies) and digested with NotI. The cDNAs were size selected by passage through cDNA size fractionation columns (Invitrogen-life technologies). The cDNAs derived from each developmental stage of a particular tissue were mixed on an equimolar basis and ligated directionally into the NotI and SalI sites of the pCMV-SPORT vector (Invitrogen). After ligation of the inserts, the plasmids were electroporated into DH10B bacteria. Library construction (PCR protocol): The amount of mRNA that was recovered from oocytes and embryos was quite limiting and was not sufficient for library production with the standard protocol. Therefore, PCR-based protocol was utilized for producing libraries from sources in which the amount of extracted mRNA was small (oocytes and embryos). Poly-A RNA was isolated by using the MicroPoly(A) Pure kit from Ambion (cat. # 1918). The mRNA was reverse transcribed with a NotI-tag-d118 oligonucleotide and a SMART oligonucleotide (Clontech) modified to contain a SalI site to generate full-length cDNA with a sequence complementary to the SMART oligonucleotide. Sequences within the SMART and dt oligonucleotides were used as primers to amplify the cDNAs by PCR with pfu turbo polymerase (Stratagene). The resulting PCR products were purified, digested with NotI and SalI and size fractionated by using Chroma Spin-1000 columns (Clontech). Purified cDNA from each PCR reaction was quantitated and mixed on an equimolar basis for ligation into the pCMV-SPORT6 vector. Preliminary library characterization: Randomly chosen clones from each library were analyzed by restriction digestion to determine average insert size (36 clones) and by sequencing (~4 96-well plates) to confirm library quality (e.g. the presence of short polyA+ tails, genomic DNA contamination (must be <1%), ribosomal RNA clones (must be <1%), etc.] and to provide a sequence

QY	361	AGAA	CAGATT	TGGAT	CTGGC	CTGCT	GAA	GCAGT	TACCT	CGAAAA	AGATTG	362			
Db	662	AAGAA	CAGATT <td>TGGAT <td>CTGGC <td>CTGCT <td>GAA <td>GCAGT <td>TACCT <td>CGAAAA <td>AGATTG</td> <td>721</td> </td></td></td></td></td></td></td>	TGGAT <td>CTGGC <td>CTGCT <td>GAA <td>GCAGT <td>TACCT <td>CGAAAA <td>AGATTG</td> <td>721</td> </td></td></td></td></td></td>	CTGGC <td>CTGCT <td>GAA <td>GCAGT <td>TACCT <td>CGAAAA <td>AGATTG</td> <td>721</td> </td></td></td></td></td>	CTGCT <td>GAA <td>GCAGT <td>TACCT <td>CGAAAA <td>AGATTG</td> <td>721</td> </td></td></td></td>	GAA <td>GCAGT <td>TACCT <td>CGAAAA <td>AGATTG</td> <td>721</td> </td></td></td>	GCAGT <td>TACCT <td>CGAAAA <td>AGATTG</td> <td>721</td> </td></td>	TACCT <td>CGAAAA <td>AGATTG</td> <td>721</td> </td>	CGAAAA <td>AGATTG</td> <td>721</td>	AGATTG	721			
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Db	722	TAGCT	CTTGAT	CCGGCA	CAAA	CAAC	ACCG	CGTGT	AGCG	TGGT	TTTTTT	TGTTG	GAA	CA	781
QY	3681	GCA	GATTAC	CGCC	CA	AAAA	AAAA	AGAT	CTTCA	GAA	GAAT	CTTTT	TGAT	CGGG	3740
Db	782	GCA	GATTAC	CGCC	CA	AAAA	AAAA	AGAT	CTTCA	GAA	GAAT	CTTTT	TGAT	CGGG	841
QY	3741	TGAC	CGTCA	GTTGA	ACGA	AAAT	CTCA	CGTTA	AGAGT	-TTT	TGCTA	TGAGT	TATC	3794	
Db	842	TGAC	CGTCA	GTTGA	ACGA	AAAT	CTCA	CGTTA	AGAGT	-TTT	TGCTA	TGAGT	TATC	896	
RESULT 14															
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DEFINITION	CB686151				925	bp	mRNA		linear		EST	09-Apr-2003			
VERSION	Bn01b_02008_A														
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SOURCE	constitutively_frost_tolerant														
ORGANISM	Brassica napus														
REFERENCE	1 (bases 1 to 925)														
AUTHORS	Singh, J., Allard, G., Tinker, N., Robert, L., Lacroix, C., De Moor, A., Chagnon, J., Farah, S., Couroux, P. and Hattori, J.														
TITLE	Expressed Sequence Tags from constitutively frost tolerant transgenic Brassica napus overexpressing BNCBP17														
JOURNAL	Unpublished (2002)														
COMMENT	Contact: Singh, J.A. Eastern Cereal and Oilseed Research Centre Agriculture and Agri-food Canada KW Neelby Bldg., Central Experimental Farm, Ottawa, Ontario, KIA 0C6, Canada Tel: (613) 759-1662 Fax: (613) 759-1701 Email: singhja@agr.gc.ca.														
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	/clone_id="Bn01b_AAPC_ECORC transgenic Brassica napus_ove"														
	repressing BNCBP17 constitutively frost tolerant"														
	/note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: EcoRI; Site 2: XhoI; Germinated in soil flats and seedlings grown for 3 weeks in a Conviron E-15 cabinet set at 20°C/16 hr light (250 Em-2sec-1) and 16 °C / 8 hr dark. Fourth leaves collected at 9 am and immediately frozen."														
ORIGIN															
Query Match	16.6%	Score	875;	DB	6;	Length	925;								
Best Local Similarity	98.6%	Pred. No.	3.4e-240;												
Matches	886;	Conservative	6;	Mismatches	6;	Indels	1;	Gaps	1;						
QY	2701	GCTG	TCTAG	AGTAT	CATG	TGTCAT	AGCTG	TTTCT	CGTGT	GAA	AAAT	TTGTT	ATCC	GTACA	2760

Db	839	ATTTCACACAAATATCGAGCCGGGAAGCATAAAGTGTAAAGCTGGGGTGGCTTAATGAGTGTG	780
QY	2821	AGCTAACTCACATTAATTATGCGTTGGCGCTCACAGCCCGCTTTCGAATCGGGAACCTGTGCG	2880
Db	779	AGCTAACTCACATTAATTATGCGTTGGCGCTCACAGCCCGCTTTCGAATCGGGAACCTGTGCG	720
QY	2881	TGCCAGCTGCAATTAATGAAATGCGCCCAACGCGCGGGGAGAGGCGGTTTTCGTAATTTGGGCGC	2940
Db	719	TGCCAGCTGCAATTAATGAAATGCGCCCAACGCGCGGGGAGAGGCGGTTTTCGTAATTTGGGCGC	660
QY	2941	TCTTCGCGTTCCTCGCTCACTGACCTCGCTGGCTTCGCTTCGTTCCGCTTCGCGCGAGCGGTA	3000
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QY	3001	TCAGCTCACTCAAAAGCGCGGTAAATACGTTATTCACAGAAATAGAGGGATATACGACAGAAAG	3060
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## JOURNAL COMMENT

Unpublished (2003)  
 Contact: Mock T  
 Biological Oceanography  
 Alfred-Wegener-Institute for Polar and Marine Research  
 Am Handelshafen 12, D-27570 Bremerhaven, Germany  
 Tel: +49 471 4831 1893  
 Fax: +49 471 4831 1425  
 Email: tmock@awi-bremerhaven.de  
 Sequence with unknown function  
 PCR Primers  
 FORWARD: 5'lambdaTriplex2  
 BACKWARD: 3'lambdaTriplex2  
 Seq primer: ctgggaagcgccatctgctgtc.  
 Location/Qualifiers

## FEATURES source

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 /note="Vector: pTriplex2; total polyA was used for first-strand synthesis with SMART IV oligos and CDS III/3'PCR primer. Double strand cDNA synthesis was done by LD PCR using the following program: 95oc for 5 min denaturation and subsequent 20 cycles at 95oc (2min) and 68oc (6min). After SfiI digestion the cDNA was fractionated with CHROMA Spin-400 columns. These cDNAs were ligated overnight into pTriplex2 vectors."

## ORIGIN

Query Match 16.4%; Score 866.2; DB 6; Length 1073;  
 Best Local Similarity 96.4%; Fred. No. 1.3e-237;  
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GenCore version 5.1.8  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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5	1602.2	30.3	5707	2	US-08-472-809B-8
6	1571.6	29.7	4665	3	US-08-948-378A-7
7	1571.6	29.7	4665	3	US-09-169-425C-7
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9	1570	29.7	4518	3	US-09-380-190A-26
10	1570	29.7	4886	3	US-09-533-220A-4
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12	1570	29.7	6139	2	US-08-751-767A-7
13	1569.8	29.7	4748	3	US-09-796-575-4
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15	1569.8	29.7	5069	3	US-09-393-483A-1
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18	1569.8	29.7	6218	3	US-09-744-016A-10
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c 26	1564.2	29.6	5532	3	US-08-961-888-40	Sequence 40, Appl
c 27	1561.4	28.4	6795	3	US-09-380-190A-22	Sequence 22, Appl
c 28	1501.4	28.4	8574	3	US-09-554-572-3	Sequence 3, Appl
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#### ALIGNMENTS

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; Sequence 16, Application US/09186002B  
; Patent No. 6489542  
; GENERAL INFORMATION:  
; APPLICANT: Corbin, David R.  
; APPLICANT: Romano, Charles P.  
; TITLE OF INVENTION: Improved Method for Transforming Plants to Express  
; FILE REFERENCE: 38-21(13547) US Pat No. 6489542 09/186,002  
; CURRENT FILING DATE: 1998-11-04  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 8349  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: gene  
; LOCATION: (3666)..(5573)  
; OTHER INFORMATION: completely synthesized  
US-09-186-002-16

Query Match 42.4%; Score 2240; DB 3; Length 8349;  
Best Local Similarity 93.4%; Pred. No. 0;  
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; Sequence 1, Application US/09554929
; Patent No. 6521427
; GENERAL INFORMATION:
; APPLICANT: Evans, Glen A.
; TITLE OF INVENTION: A Method for the Complete Chemical
; FILE REFERENCE: P-EA 4749
; CURRENT APPLICATION NUMBER: US/09/554, 929
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4800
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic plasmid
US-09-554-929-1

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Qy      3487 AGGATTAAGCAGAGGATATATAGGCGGTCTACAGATTTCTGAAGTGTGCGCTTAC 3546
Db      4440 AGGATTAAGCAGAGGATATATAGGCGGTCTACAGATTTCTGAAGTGTGCGCTTAC 4381
Qy      3547 TACGCTACACTAGAGACAGTATTTGATCTGCGCTGCTGAGGAGCAGTTACCTTC 3606
Db      4380 TACGCTACACTAGAGACAGTATTTGATCTGCGCTGCTGAGGAGCAGTTACCTTC 4321
Qy      3607 GGAAGAAAGATTGATCTTGTATCCGGAACAAACCAACCGCTGTAGCGGTGTTT 3666
Db      4320 GGAAGAAAGATTGATCTTGTATCCGGAACAAACCAACCGCTGTAGCGGTGTTT 4261
Qy      3667 TTGTTTGAAGGACGAGTTACGCGGAGAAAAAGATCTCAAGAAATCTTTGATC 3726
Db      4260 TTGTTTGAAGGACGAGTTACGCGGAGAAAAAGATCTCAAGAAATCTTTGATC 4201

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Qy      3727 TTTTCTACGGGCTGACGCTCAGTGAACGAAAACTCAGTTAAGGATTTTGTGATG 3786
Db      4200 TTTTCTACGGGCTGACGCTCAGTGAACGAAAACTCAGTTAAGGATTTTGTGATG 4142
Qy      3787 AGATTAATGTCACCAAGCGGCGATGTGCTCCCACTTCGCAATTCGGGGGCGATG 3846
Db      4141 ----- 4142
Qy      3847 ATGGCGGATAGCGCGCTGTGTTTCTCGATGCGGACGATTTGCACTGCGGATAGAC 3906
Db      4141 ----- 4142
Qy      3907 TCCGCGAGTGTGTCAGGCTCAGGACGAGCTGAACCAACTCGGAGGAGATCGAGCCG 3966
Db      4141 -----GCCCG 4137
Qy      3967 GGGTGGCGAAGAACTCCAGATGATATCCCGGCTGAGAGATCATCCAGCCGCGTCC 4026
Db      4136 GGGTGGCGAAGAACTCCAGATGATATCCCGGCTGAGAGATCATCCAGCCGCGTCC 4077
Qy      4027 CGGAAACGATTTCCGAAGCCCACTTTCTATGAAGCGGCGGTGGAATCGAAATCTTGT 4086
Db      4076 CGGAAACGATTTCCGAAGCCCACTTTCTATGAAGCGGCGGTGGAATCGAAATCTTGT 4017
Qy      4087 GATGCGAGTTGGGCGTCCGCTGATGATTTGCAATCCAGATCCGCTCAGAAAG 4146
Db      4016 GATGCGAGTTGGGCGTCCGCTGATGATTTGCAATCCAGATCCGCTCAGAAAG 3957
Qy      4147 ACTGTCAGAAAGCGATAGAAAGCGATGCGCTGCGATCGGAGCGGCGATACCGTAAA 4206
Db      3956 ACTGTCAGAAAGCGATAGAAAGCGATGCGCTGCGATCGGAGCGGCGATACCGTAAA 3897
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Db      3896 GCACAGAAAGCGGTGACGCCCATTCGCGGCAAGCTTTGACGAAATTCACGGGTAGCCA 3837
Qy      4267 ACGCTATGTCTGATAGCGGTCGCGCACACCGCGGCGGCGGCGATGATGATGATCAGAAA 4326
Db      3836 ACGCTATGTCTGATAGCGGTCGCGCACACCGCGGCGGCGGCGATGATGATGATCAGAAA 3777
Qy      4327 AGCGGCAATTTTCAACCATGATATTCGCGAAGCAGGATCGCATGAGTACGAGAT 4386
Db      3776 AGCGGCAATTTTCAACCATGATATTCGCGAAGCAGGATCGCATGAGTACGAGAT 3717
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Qy      4447 GATGCTCTTCTGTCAGATCATCTGATGCAAGAAACCGGCTTCATCCAGATAGTGTCTC 4506
Db      3656 GATGCTCTTCTGTCAGATCATCTGATGCAAGAAACCGGCTTCATCCAGATAGTGTCTC 3597
Qy      4507 GCTCGATGCGATGTTTGTGCTGTGATGGAATGGGCGAGTATGCGGATCAAGCGTATGCA 4566
Db      3596 GCTCGATGCGATGTTTGTGCTGTGATGGAATGGGCGAGTATGCGGATCAAGCGTATGCA 3537
Qy      4567 GCGCGCGCATTTGATCATGAGCATGATGATATCTTTCTCGGCGAGGACGAAAGTATGACA 4626
Db      3536 GCGCGCGCATTTGATCATGAGCATGATGATATCTTTCTCGGCGAGGACGAAAGTATGACA 3477
Qy      4627 GGAATCCGTCGCGCGGACCTTGGCCCAATAGCAGCAGTCCCTTCCGCTTCAGTGAACA 4686
Db      3476 GGAATCCGTCGCGCGGACCTTGGCCCAATAGCAGCAGTCCCTTCCGCTTCAGTGAACA 3417
Qy      4687 CGTGAGCAGAGCTGCGCAAGAAACCGCGTGTGCGCAGCAGATGACCGGCTGCTC 4746
Db      3416 CGTGAGCAGAGCTGCGCAAGAAACCGCGTGTGCGCAGCAGATGACCGGCTGCTC 3357
Qy      4747 CGTCTGCAATTTATTCAGGCGACCGGACAGGTGCGTCTTGAACAAAAGAACCGGCGCC 4806
Db      3356 CGTCTGCAATTTATTCAGGCGACCGGACAGGTGCGTCTTGAACAAAAGAACCGGCGCC 3297
Qy      4807 CTGCGCTGACAGCGGAAACAGCGGCGCATCAAGACAGCGGATTTGTGTGTGCCAGT 4866

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Db 3296 CCGGCGGTGACGCGGAGACGCGGCGATCAGAGACCGGATGCTGTGGCCCACT 3237  
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Db 3236 CATAGCGGATAGCCTCTCCACCAGCGCGGAGACCTGCTGCAATCCATCTTGT 3177  
QY 4927 CAATCATGCAAAAGCATCTCATCTCTCTTGTAGTCAAGTCTTATCCCGCGGCATC 4986  
Db 3176 CAATCATGCAAAAGCATCTCATCTCTCTTGTAGTCAAGTCTTATCCCGCGGCATC 3117  
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QY 5047 AGGCGCGCCGAGCTGGCAATTCGGTTCGCTTGTCTGCTTAAACCGCCCACTAGCT 5106  
Db 3056 AGGCGCGCCGAGCTGGCAATTCGGTTCGCTTGTCTGCTTAAACCGCCCACTAGCT 2997  
QY 5107 ATGCGCATGTAGGCGCATGCAAGCTACTGCTTCTCTTGGCGCTTGTTCCTTG 5166  
Db 2996 ATGCGCATGTAGGCGCATGCAAGCTACTGCTTCTCTTGGCGCTTGTTCCTTG 2937  
QY 5167 TCCAGATAGCCGAGTACGATCATTCATTCGGGGGTCAACACGTTTTCGCGACTGGCT 5226  
Db 2936 TCCAGATAGCCGAGTACGATCATTCATTCGGGGGTCAACACGTTTTCGCGACTGGCT 2877  
QY 5227 TCTACGTGTTCGGCTCTCTTAGACGCGCTTGGCGCGCTTGGAGTGTTCGCGAGCGTG 5283  
Db 2876 TCTACGTGTTCGGCTCTCTTAGACGCGCTTGGCGCGCTTGGAGTGTTCGCGAGCGTG 2820

## RESULT 3

US-09-380-190A-29/c  
Sequence 29, Application US/09380190A

Patent No. 6410220  
GENERAL INFORMATION:

APPLICANT: NATURE TECHNOLOGY CORPORATION, ET AL.  
TITLE OF INVENTION: SELF-ASSEMBLING GENES, VECTORS AND USES  
THERBOF

NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:

ADDRESSEE: MUEITING, RAASCH & GRUBHARDT, P.A.  
STREET: 119 NORTH FOURTH STREET, SUITE 203  
CITY: MINNEAPOLIS  
STATE: MINNESOTA  
COUNTRY: USA

ZIP: 55401  
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/380,190A  
FILING DATE: 26-Aug-1999

CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US98/03918

FILING DATE: 28-FEB-98  
ATTORNEY/AGENT INFORMATION:  
NAME: MUEITING, ANN M.  
REGISTRATION NUMBER: 33,977

REFERENCE/DOCKET NUMBER: 228, 00010201  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-305-1217  
TELEFAX: 612-305-1228

INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5594 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 29:  
US-09-380-190A-29

Query Match 31.3%; Score 1652.4; DB 3; Length 5594;  
Best Local Similarity 85.4%; Pred. No. 0;  
Matches 1916; Conservative 0; Mismatches 261; Indels 67; Gaps 4;

QY 3107 CCGGCTTGGCGCTTTTTCATAGGCTCCGCCCTGACGAGCATCACAAAATGAC 3166  
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QY 3167 GCTCAATCAGAGTGGCGAAACCCGACAGAGCTATAAGTACAGGCTTCCCTG 3226  
Db 5531 GCTCAATCAGAGTGGCGAAACCCGACAGAGCTATAAGTACAGGCTTCCCTG 5472  
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QY 3347 TGTAGTGTTCGCTCAAGCTGGGCTGTGTGACGAACCCCGCTTACGCCGACGCT 3406  
Db 5351 TGTAGTGTTCGCTCAAGCTGGGCTGTGTGACGAACCCCGCTTACGCCGACGCT 5292  
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Db 5291 GCGCTTATCCGTAATCTATGTCTTGAAGTCCAAACCGGTAAAGACACTTATCGCAC 5232  
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Db 5231 TGGCAGCGGCACTGTAAAGAGATTAGCAGAGGATATGAGCGGTCTACAGGT 5172  
QY 3527 TCTTGAAGTGTGGCTTAATCGGCTACACTAGAAACAGATATTGTGTATCGCGTC 3586  
Db 5171 TCTTGAAGTGTGGCTTAATCGGCTACACTAGAAACAGATATTGTGTATCGCGTC 5112  
QY 3587 TGTGAAGCACTTACCTTCGGAAGAGGTGTGAGCTCTTGAATCCGCAAAACCA 3646  
Db 5111 TGTGAAGCACTTACCTTCGGAAGAGGTGTGAGCTCTTGAATCCGCAAAACCA 5052  
QY 3647 CCGCTGTAGCGGTGTTTTTTTGTGCAACAGCAATTCGCGCAAAAAGAT 3706  
Db 5051 CCGCTGTAGCGGTGTTTTTTTGTGCAACAGCAATTCGCGCAAAAAGAT 4992  
QY 3707 CTCAGAGATCTTGAATCTTTTCTAGCGGCTCTGACGCTC-----AGTGAAGC 3757  
Db 4991 GGTGTGGGCTCTTTTATTGAGCTCGGAGAGAGAGCGCGGAACAGAGAGAGAGCG 4932  
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Db 4931 AACTGATGTTAGTTCAATAAGGACAGGCTCATTTCAAGCTCTTGGGAGCACCTGGA 4872  
QY 3818 CTC-----CCACCTCTGCAATTTGGGGGATGATCGCGGATAGCGCGC 3864  
Db 4871 AACTGATGATGTTCTCTAGAAATGCTGAGGCTGAGACGATCTGGGACATCTGTT 4812  
QY 3865 CTGTTTTCTGATGTCGACGATTTG-----ACTCGGATAGAACTCGCGAG 3914  
Db 4811 CTGTTGCTGATGTCGACGATTTG-----ACTCGGATAGAACTCGCGAG 4752  
QY 3915 GTGTCAGGCTCAGGACAGCTGAACCAACTCGGAGGATTCGACCCCGGGTGGG 3974  
Db 4751 GTGTCAGGCTCAGGACAGCTGAACCAACTCGGAGGATTCGACCCCGGGTGGG 4692  
QY 3975 GAAGAACTCAGCATGATCCCGGCTGAGAGATCATCAGCGCGCTCCCGAAAC 4034  
Db 4691 TTGGCCCATATTTCAGCTGTTCATCTGTCTGACCTTGAATGAACTTCTATTC 4632  
QY 4035 GATTCGAAAGCCCAACTTTCATAGAAAGCGGAGTGAATGAAATTCG----- 4085





Db	2185	ATTAAGATACCAGGCGGTTCCCTCGAAGCTCCCTGTGGGCTCTCTCTCCGACCT	2126
Qy	3361	GCCTCTTACCGGATACCTGTCCGCTTCTCCCTTCGGAAGCGTGGCGCTTCTCATAG	3320
Db	2125	GCCCTTACCGGATACCTGTCCGCTTCTCTCTCCGGAAGCGTGGCGCTTCTCATAG	2066
Qy	3321	CTCAGCGTGAAGATATCTCACTTGGGTGATGTCTTCCCTCAAGCTGGGCTGTGTGA	3380
Db	2065	CTCAGCGTGAAGATATCTCACTTGGGTGATGTCTTCCCTCAAGCTGGGCTGTGTGA	2006
Qy	3381	CGAACCCCGCTTACGCCCGACCGCTGCGCTTATCCGATACATTCCTTGAAGTCCA	3440
Db	2005	CGAACCCCGCTTACGCCCGACCGCTGCGCTTATCCGATACATTCCTTGAAGTCCA	1946
Qy	3441	CCCGGTAAACAAGATTAATCGCACTGGCAGACGCCACTGTAAACAGATTAGCAGAC	3500
Db	1945	CCCGGTAAACAAGATTAATCGCACTGGCAGACGCCACTGTAAACAGATTAGCAGAC	1886
Qy	3501	GAGTATGTAGGCGGTGCTACAGATTCTTGAAGTGTGGCCCTAACTAGCGCTACCTAG	3560
Db	1885	GAGTATGTAGGCGGTGCTACAGATTCTTGAAGTGTGGCCCTAACTAGCGCTACCTAG	1826
Qy	3561	AAGAACAATTTTGTGATCTGCGCTGTGCTGAAGCCAGTTACCTTCGAAAAAGATTGG	3620
Db	1825	AAGAACAATTTTGTGATCTGCGCTGTGCTGAAGCCAGTTACCTTCGAAAAAGATTGG	1766
Qy	3621	TAGCTCTGATCCGGGAAACAACCAACCGCTGTACCGGTGTGTTTTTGTTCGAAGA	3680
Db	1765	TAGCTCTGATCCGGGAAACAACCAACCGCTGTACCGGTGTGTTTTTGTTCGAAGA	1706
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Db	1705	GCAGATTACGCGCAGAAAAAAGATCTGAAGAATCTTTGATCTTTCTACGGGGTTC	1696
Qy	3741	TGACGCTCAGTGAACGAAAACTCACGTTAAAGGATTTTGTGATGATTAATCGTCAAC	3800
Db	1695	TGACGCTCAGTGAACGAAAACTCACGTTAAAGGATTTTGTGATGATTAATCGTCAAC	1696
Qy	3801	CAAAAGCGCATCTGCTCTCCCACTCTGAGTTCCGGGGCATGATGCGCGATAGCC	3860
Db	1695	CAAAAGCGCATCTGCTCTCCCACTCTGAGTTCCGGGGCATGATGCGCGATAGCC	1696
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Db	1695	GCTGCTGTTTCTGGATGCCACGGAATTGCACTGCCGTTAAGAACTCCGAGAGTCTTC	1696
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Db	1695	CAGCTCAGGACAGCTGAACCACTGCGAGGGATTCAGCCCCGGGGTGGGGAGAA	1695
Qy	3981	CTCCAGCATGAGATCCCGCGCTGGAGATCATCGCCGCGCTCCGGAAAAAGATTCC	4040
Db	1674	CTCCAGCATGAGATCCCGCGCTGGAGATCATCGCCGCGCTCCGGAAAAAGATTCC	1615
Qy	4041	GAAAGCCAACTTTCATAGAAGGCGCGGTGAATCGAAATCTGTGATGCGACAGTTGGG	4100
Db	1614	GAAAGCCAACTTTCATAGAAGGCGCGGTGAATCGAAATCTGTGATGCGACAGTTGGG	1555
Qy	4101	CGTGGCTTGTGCGGTCAATTTGAAACCCAGAGTCCCGCTCAGAAAGAACTGTCAAAGAG	4160
Db	1554	CGTGGCTTGTGCGGTCAATTTGAAACCCAGAGTCCCGCTCAGAAAGAACTGTCAAAGAG	1495
Qy	4161	CGATAGAAGCGATGCGGTGCGAATCGGGAAGGCGCGATCCGTAAACGAGAGAGCGG	4220
Db	1494	CGATAGAAGCGATGCGGTGCGAATCGGGAAGGCGCGATCCGTAAACGAGAGAGCGG	1435
Qy	4221	TCAGCCATTCGCGCGCAAGCTTTCAGCAATATCAAGGTAGGCAACGCTATGTCTGA	4280
Db	1434	TCAGCCATTCGCGCGCAAGCTTTCAGCAATATCAAGGTAGGCAACGCTATGTCTGA	1375
Qy	4281	TAGCGGTTCGCGCAACCGCGCGCAAGTCCATGAATCCAGAAAAAGCGCAATTTTCC	4340
Db	1374	TAGCGGTTCGCGCAACCGCGCGCAAGTCCATGAATCCAGAAAAAGCGCAATTTTCC	1315
Qy	4341	ACCATGATATTCCGCAAGCAGGCAATCGCATGGGTCAAGAGATCTTCGCGGTGGGC	4400
Db	1314	ACCATGATATTCCGCAAGCAGGCAATCGCATGGGTCAAGAGATCTTCGCGGTGGGC	1255
Qy	4401	ATGCGCGCTTGAAGCTTGGCAGACAGTTCCGCTGCGCGAGCCCTGATGCTTTCGTC	4460
Db	1254	ATGCGCGCTTGAAGCTTGGCAGACAGTTCCGCTGCGCGAGCCCTGATGCTTTCGTC	1195
Qy	4461	AGATCATCTGATGACAAAGCCGCTTTCATCCAGTACGCTGCTGATGCGATGT	4520
Db	1194	AGATCATCTGATGACAAAGCCGCTTTCATCCAGTACGCTGCTGATGCGATGT	1135
Qy	4521	TTGCTTGGTGGTGAATGGGCAAGTGGCGGATGCAAGCCTATGACGCGCCCATTTGA	4580
Db	1134	TTGCTTGGTGGTGAATGGGCAAGTGGCGGATGCAAGCCTATGACGCGCCCATTTGA	1075
Qy	4581	TCAGCCATGATGATCTTTCGCGCAGAGCAAGGTGAGATGACAGAGATCTGCCCC	4640
Db	1074	TCAGCCATGATGATCTTTCGCGCAGAGCAAGGTGAGATGACAGAGATCTGCCCC	1015
Qy	4641	GGCATTGGCCCAATAGACGAGTCCCTCCGCTTCACTGCAACCTGTGACACAAGCT	4700
Db	1014	GGCATTGGCCCAATAGACGAGTCCCTCCGCTTCACTGCAACCTGTGACACAAGCT	955
Qy	4701	GCGCAAGAACCGCCGCTGTGGGCAAGCATAGCCGCTGCTCTGCTTCAGTTCA	4760
Db	954	GCGCAAGAACCGCCGCTGTGGGCAAGCATAGCCGCTGCTCTGCTTCAGTTCA	895
Qy	4761	TTGAGGGCACCGGACAGGTGGTCTTGACAAAAAGAACCGGGCGCCCTGCGCTGACG	4820
Db	894	TTGAGGGCACCGGACAGGTGGTCTTGACAAAAAGAACCGGGCGCCCTGCGCTGACG	835
Qy	4821	CGAACAACCGGCGCATCAGAGCAGCGATGTCTGTGGCCAGCATAGCGGAATAGC	4880
Db	834	CGAACAACCGGCGCATCAGAGCAGCGATGTCTGTGGCCAGCATAGCGGAATAGC	775
Qy	4881	CTCTCAACCAAGCGGCGGAGAACTCGGTGCAATCATCTTGTTCATATGCGAAAC	4940
Db	774	CTCTCAACCAAGCGGCGGAGAACTCGGTGCAATCATCTTGTTCATATGCGAAAC	715
Qy	4941	GATCTCATCTGTCTCTTGATCAGATCTTGAATCCCTGCGGCATCAGATCCTTGGCGGC	5000
Db	714	GATCTCATCTGTCTCTTGATCAGATCTTGAATCCCTGCGGCATCAGATCCTTGGCGGC	655
Qy	5001	AAGAAAGCATTCAGTTTACTTTGAGGGCTTCCCACTTACAGAGGCGGCCAGCT	5060
Db	654	AAGAAAGCATTCAGTTTACTTTGAGGGCTTCCCACTTACAGAGGCGGCCAGCT	595
Qy	5061	GGCAATTCGCTTGGCTGCTGCTGCAATAAACCGGCCAGTCAAGTATTCGATTAAGC	5120
Db	594	GGCAATTCGCTTGGCTGCTGCTGCTGCAATAAACCGGCCAGTCAAGTATTCGATTAAGC	535
Qy	5121	CCAAGCAAGTACTGCTTCTCTTGGCGCTTGGCGTTTCCCTTGTCCAGATAGCCAG	5180
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Qy	5		

APPLICANT: Demayo, Franco J.  
APPLICANT: O'Malley, Bert W.  
TITLE OF INVENTION: Expression Vector Systems and  
TITLE OF INVENTION: Method of Use  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESS: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: Storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/472,809B  
FILING DATE: June 7, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/209,846  
FILING DATE: March 9, 1994  
APPLICATION NUMBER: 07/789,919  
FILING DATE: No. 592554ember 6, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Wardburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 214/212  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5707 bases  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-472-809B-8

Query Match 30.3%; Score 1602.2; DB 2; Length 5707;  
Best Local Similarity 82.8%; Pred. No. 0;  
Matches 2021; Conservative 0; Mismatches 28; Indels 392; Gaps 1;

QY 2706 CTAGACGTAATCATGTCATGCTGTTCCGTGTAATAATTGTTATCCGCTCACAATTCC 2765  
DB 3514 CTTGGCTATCATGTCATGCTGTTCTGTGTAATGTTATCCGCTCACAATTCC 3573  
QY 2766 ACACAAATACGAGCCGGAAGCATTAAGTGAAGCCCTGAGGCTCTAATAGTAGCTA 2825  
DB 3574 ACACAAATACGAGCCGGAAGCATTAAGTGAAGCCCTGAGGCTCTAATAGTAGCTA 3633  
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DB 3754 CGCTTCCTGCTCACTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3813  
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DB 3994 AAACCCGACAGAGCTATAAATATACAGGCGTTTCCCTTGAAAGCTCCCTGTCGCTC 4053  
QY 3246 TCGTGTCCGACCGCTGCGCTTACCGGATACCTGTCGCTTTCCCTTGCGGAGGCT 3305  
DB 4054 TCGTGTCCGACCGCTGCGCTTACCGGATACCTGTCGCTTTCCCTTGCGGAGGCT 4113  
QY 3306 GGGCGCTTCTCATAGCTCAAGCTGTAAGTATCTGAGTTCGCTGCTGCTGCA 3365  
DB 4114 GGGCGCTTCTCATAGCTCAAGCTGTAAGTATCTGAGTTCGCTGCTGCTGCA 4173  
QY 3366 GCTGGGCTGTGACAGAACCCCGCTTACGCGCCGACCGCTGCGCTTATCCGTTACTA 3425  
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QY 3426 TCGTCTTGAAGTCAACCCGCTGTAAGACAGCACTTATCCGCACTGGGAGCGCACTGTA 3485  
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QY 3486 CAGGATTAGCAGAGCGAGATATGAGCGGTGCTACAGAGTTCTTGAAGTGAGGCTTAA 3545  
DB 4294 CAGGATTAGCAGAGCGAGATATGAGCGGTGCTACAGAGTTCTTGAAGTGAGGCTTAA 4353  
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DB 4474 TTTTGTTCGAGCAGAGATTAAGCGCAGAAAAAGATCTCAAGAAAGATCTTTGAT 4533  
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DB 4534 CTTTCTTACGCGGCTGACGCTCAGTGGAACGAAACTCACGTTAAGGATTTTGTCAT 4551  
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DB 4552 ----- 4551  
QY 3846 GATGCGGATAGCCGCTGCTGTTCTCGGATGCGACGGAATTTGCACTGCCGTAGAA 3905  
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QY 3966 GGGGTGGGAGAAACTCAGCATGAGATCCCGCGCTGAGAGATCATTCAGCCGGGCTC 4025  
DB 4552 ----- 4551  
QY 4026 CCGAAAAAGATTCCGAAGCCCAACTTTGATGAAGCGCGGTGGAATCGAATCTCG 4085  
DB 4552 ----- 4551  
QY 4086 TGATGCGAGTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4145  
DB 4552 -----CGCTCAGAAAG 4561  
QY 4146 AACCTCGCAAGAAAGGCGATGAAAGGCGATGCGTGGCAATCGGAGGCGGATACGTTA 4205

Db 4562 AACCTGCAAGAGGCGATGAGAGGCGATCGCTGCGAATCGGAGGCGGATACCGTAA 4621  
Qy 4206 AGCAGAGGAAAGCGGTCAAGCCCATTCGCCCGCAAGCTCTTACACATATACAGGTAGCC 4265  
Db 4622 AGCAGAGGAAAGCGGTCAAGCCCATTCGCCCGCAAGCTCTTACACATATACAGGTAGCC 4681  
Qy 4266 AACGCTATGCTCTGATAGCGGTCCGCGACACCCAGCGCGACAGTGCATGAATCCAGAA 4325  
Db 4682 AACCTATGCTCTGATAGCGGTCCGCGACACCCAGCGCGACAGTGCATGAATCCAGAA 4741  
Qy 4326 AAGCGGCGATTTTCCACCATATATTCGGCAAGAGGATTCGCATGGGTCAAGACAGA 4385  
Db 4742 AAGCGGCGATTTTCCACCATATATTCGGCAAGAGGATTCGCATGGGTCAAGACAGA 4801  
Qy 4386 TCCTCGCGGTGGGAGTGGCGGCTTGAAGCTTGGCGAAGTTTCGGTGGCGCGAGCCCG 4445  
Db 4802 TCCTCGCGGTGGGAGTGGCGGCTTGAAGCTTGGCGAAGTTTCGGTGGCGCGAGCCCG 4861  
Qy 4446 TGATGCTCTTCTGTCAGATCATCTGATCGAAGAACCGGCTTCCATCCGAGTACGTGCT 4505  
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Qy 4506 CGCTGATGCGATGTTTGGCTTGGTGGTTCGAATGGGAGGTAAGCGGATCAAGCGTATGC 4565  
Db 4922 CGCTGATGCGATGTTTGGCTTGGTGGTTCGAATGGGAGGTAAGCGGATCAAGCGTATGC 4981  
Qy 4566 AGCGCGCGATTTGATCGACCATGATGATGATCTTCTTCGCGAGAGCAAGGTGATGATAC 4625  
Db 4982 AGCGCGCGATTTGATCGACCATGATGATGATCTTCTTCGCGAGAGCAAGGTGATGATAC 5041  
Qy 4626 AAGAGATCTTCGCGCGGCACTTTCGCGCAATAGCAAGCCAGTCCCTTCCGCTTCACTGACA 4685  
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Qy 4806 CCTCGCGTGAACGCGCGAACAACGCGCGCATTCAGAGGCGCGATTTGTTGGGCCAG 4865  
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Db 5522 AACTGTGGGAAAGGCGAATCGGTGCGGCTCTTTCGCTAAT 5562

RESULT 6  
US-08-948-378A-7/c  
; Sequence 7, Application US/08948378A  
; Patent No. 6013258  
; GENERAL INFORMATION:

APPLICANT: Urban, Robert G.  
APPLICANT: Chicz, Roman M.  
APPLICANT: Collins, Edward J.  
APPLICANT: Hedley, Mary Lynn  
TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM  
TITLE OF INVENTION: THE HPV E7 PROTEIN  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
FILING DATE: 09-OCT-1997  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER:  
ATTORNEY/AGENT INFORMATION:  
NAME: Frazer, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 08191/004001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-543-8906  
TELEX: 200154  
INFORMATION FOR SEQ. ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4665 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: circular  
MOLECULE TYPE: PHOTOPHPV  
US-08-948-378A-7  
Query Match 29.7%; Score 1571.6; DB 3; Length 4665;  
Best Local Similarity 86.3%; Pred. No. 0;  
Matches 1850; Conservative 0; Mismatches 114; Indels 180; Gaps 3;  
Qy 3008 ACTCAAGCGGTAAATACGTTATCCACAGATCAGGGGATTAACGAGGAAAGAAATAT 3067  
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 DB 1844 GATTATCAAAAAGATCTTCACTGATCTTTAAATTAATAAGATTTTAATGA 1785  
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 QY 3901 -----TAGAACTCCGCGAGTCTGCTCAAGCCTCAGCAGCAGCTGAACCAAC 3946  
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 QY 3947 TCGGAGAGGATCGA----- 3961  
 DB 1604 CCGCGCTTATGAACCAACCAACCAACCGGCTTATCTGCTTTTATGCGG 1545  
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 QY 4148 CTGCTCAAGAAAGCGATAGAGCGATGCGCTGCGAATCCGGAAGCGGGAATACGTTAAG 4207  
 DB 1304 CTGCTCAAGAAAGCGATAGAGCGATGCGCTGCGAATCCGGAAGCGGGAATACGTTAAG 1245  
 QY 4208 CACGAGAAAGCGCTCAGCCCATTTGCGCGCAAGCTCTTCAAGCAATATCACGGGTAGCAA 4267  
 DB 1244 CACGAGAAAGCGCTCAGCCCATTTGCGCGCAAGCTCTTCAAGCAATATCACGGGTAGCAA 1185  
 QY 4268 CGCATATGCTCGATAGAGGCTCCGCAACCAAGCGCGCAGCAGTCAATGATCCAGAAA 4327  
 DB 1184 CGCATATGCTCGATAGAGGCTCCGCAACCAAGCGCGCAGCAGTCAATGATCCAGAAA 1125

QY 4328 GCGGCCATTTTTCACCATGATATTTGGCAGAGGCAATGCGCATGGGTGCACAGCAGATC 4387  
 DB 1124 GCGGCCATTTTTCACCATGATATTTGGCAGAGGCAATGCGCATGGGTGCACAGCAGATC 1065  
 QY 4388 CTGCGCGTGGGCAATGCGCGCTTGAAGCTTGGCCAAAGTTTGGCTGGCGGAGCCCTTG 4447  
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 QY 4448 ATGCTCTTGTGCAAGATCATCTGATGCAAGAGCCGCTTCCATCCAGATACGTGCTCG 4507  
 DB 1004 ATGCTCTTGTGCAAGATCATCTGATGCAAGAGCCGCTTCCATCCAGATACGTGCTCG 945  
 QY 4508 CTCGATGCGATGTTTCTGCTGTGTGCTCAATAGGCGAGTACCGGATCAAGCTATGAG 4567  
 DB 944 CTCGATGCGATGTTTCTGCTGTGTGCTCAATAGGCGAGTACCGGATCAAGGATGAG 885  
 QY 4568 CCGCGCATTTGATCAGGCATGATGATGATCTTTCTGCGCAGAGCAGAGTATGATGAG 4627  
 DB 884 CCGCGCATTTGATCAGGCATGATGATGATCTTTCTGCGCAGAGCAGAGTATGATGAG 825  
 QY 4628 GAGATCTTGGCCCGGCACTTGGCCCAATAGAGCAGAGCTTCCGCTTCAATGACAAAC 4687  
 DB 824 GAGATCTTGGCCCGGCACTTGGCCCAATAGAGCAGAGCTTCCGCTTCAATGACAAAC 765  
 QY 4688 GTGAGCAGACAGCTGCGCAGAGAACGCGCTGTGAGCAGCAGATAGCCGCTGCTC 4747  
 DB 764 GTGAGCAGACAGCTGCGCAGAGAACGCGCTGTGAGCAGCAGATAGCCGCTGCTC 705  
 QY 4748 GTCTGCAATTCATTCAGGGGCAACCGGACAGGTGCTTGAACAATAAGAACCGGGCGCC 4807  
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 QY 4808 CTGCGCTGACAGCGCGGAAACAGGGGATCAGAGCAGCCGATTTCTGTTGCTGCAATC 4867  
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 DB 584 ATAGCCGATATGCTTCCACCCCAAGCGCGGAGAACTGCGGCAATCATCTTGTTC 525  
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 DB 524 AATCATCGAAACGATCTCATCTGCTTGAATCAGATCTTG 481

RESULT 7  
 US-09-169-425C-7/c  
 : Sequence 7, Application US/09169425C  
 : Patent No. 6183746  
 : GENERAL INFORMATION:  
 : APPLICANT: Urban, Robert G.  
 : APPLICANT: Chiez, Roman M.  
 : APPLICANT: Collins, Edward J.  
 : APPLICANT: Hedley, Mary Lynn  
 : TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7  
 : NUMBER OF SEQUENCES: 33  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Fish & Richardson, P.C.  
 : STREET: 225 Franklin Street  
 : CITY: Boston  
 : STATE: MA  
 : COUNTRY: US  
 : ZIP: 02110-2804  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Diskette  
 : COMPUTER: IBM compatible  
 : OPERATING SYSTEM: Windows95  
 : SOFTWARE: FastSeq for Windows Version 2.0  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/09/169,425C  
 : FILING DATE: 09-OCT-1998  
 : PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/061,657  
FILING DATE: 09-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 08191/004002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-543-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4665 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-09-169-425C-7

Query Match 29.7%; Score 1571.6; DB 3; Length 4665;  
Best Local Similarity 86.3%; Pred. No. 0; Mismatches 114; Indels 180; Gaps 3;  
Matches 1850; Conservative 0;

QY 3008 ACTCAAGCGGTATACGGTTATCCAGAAATCAGGGGATTAACGAGAAAGAACATGT 3067  
DB 2624 AATGCATGGCGGTATACGGTTATCCACAGATCAGGGGATTAACGAGAAAGAACATGT 2565  
QY 3068 GAGCAAAAGCCACGCAAAAGCCACGAAACCGTAAAAAGCCGCTGCTGCTGCTTTTCC 3127  
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DB 1904 TTTCTACGGGCTGACGCTCAGTGAACGAAAACTCAGTTAAGGATTTTGTCTATGA 1845  
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QY 3947 TCGCAGGGGATCGA----- 3961  
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QY 4088 ATGCAAGTTGGGCTGCTGCTGCTGCTATTTGCAACCCAGAGTCCGCTCAAGAA 4147  
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QY 4568 CCGCCGATTTGATCAGCATGATGATCTTTCTCGGAGAGCAAGGTGATGACAG 4627  
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QY 4628 GAGATCTTGGCCGCACTTGGCCAAATAGACAGCTCCCTTCCGCTTCAAGTCAAC 4687  
DB 824 GAGATCTTGGCCGCACTTGGCCAAATAGACAGCTCCCTTCCGCTTCAAGTCAAC 765











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Db 2915 CACGAGGAAGCGGTGACCCCATTCGCGCGCAAGCTTTCAGCAATATCAAGGTAACCA 2856  
QY 4268 CGCTATGCTCTGATAGCGGTCCGCAACACCGCGCAACAGTCGATGAATCCAGAAA 4327  
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; Sequence 4, Application US/10128853
; Patent No. 6887978
; GENERAL INFORMATION:
; APPLICANT: James, Iain Fraser
; TITLE OF INVENTION: Human Vanilloid Receptor
; FILE REFERENCE: 4-30875A
; CURRENT APPLICATION NUMBER: US/10/128, 853
; PRIOR FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US/09/533,220
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: UNITED KINGDOM 9907097.1
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 1.30
; SEQ ID NO 4
; LENGTH: 4886
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-128-853-4

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Query Match 29.7%; Score 1570; DB 3; Length 4886;

Best Local Similarity 86.2%; Pred. No. 0;

Matches 1849; Conservative 0; Mismatches 115; Indels 180; Gaps 3;

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DB 3393 TGGGCTGTGTCAGAAACCCCGCTTACGCGCGCTGCGCTTATCCGGTAACTATC 3876
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DB 3275 CCCCAGTTTATGAACAAACAGACCAACACCGTTCCTTATTTCTGCTTTTATTTGCGG 3216
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Db 2495 GAGATCTGCCCCGGGCACTTCGCGCAATGACACAGTCCCTTCGCGCTTCAATGACAC 2436  
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Db 2255 ATAGCCGATAGCTCTCCACCCAGCGCGGAGAACTGCTGCAATCATCTGTTTC 2196  
Qy 4928 AATCATGCGAAAGATCTCATCTGCTTGTATCATCATCTTG 4971  
Db 2195 AATCATGCGAAAGATCTCATCTGCTTGTATCATCATCTTG 2152

## RESULT 12

US-08-751-767A-7/C  
; Sequence 7, Application US/08751767A  
; Patent No. 5994104  
; GENERAL INFORMATION:  
; APPLICANT: ANDERSON, ROBERT J.  
; APPLICANT: GRANT, HUGH  
; APPLICANT: MACDONALD, IAN D.  
; TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN  
; NUMBER OF SEQUENCES: 80  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYTE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/751,767A  
; FILING DATE: 08-NOV-1996  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SADOFF, B.J.  
; REGISTRATION NUMBER: 36,663  
; REFERENCE/DOCKET NUMBER: 117-221  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 7038164091  
; TELEFAX: 7038164100  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6139 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 3222..4841  
US-08-751-767A-7

Query Match 29.7%; Score 1570; DB 2; Length 6139;  
Best Local Similarity 86.2%; Pred. No. 0;  
Matches 1849; Conservative 0; Mismatches 115; Indels 180; Gaps 3;

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Db 2888 TCGAAGACATCTCATCTCTCTCTTGTGATCAATCTTG 2850

RESULT 15  
US-09-393-483A-1/C  
; Sequence 1, Application US/09393483A  
; Patent No. 6689936  
; GENERAL INFORMATION:  
; APPLICANT: Burgeson, Robert  
; APPLICANT: Amano, Satoshi  
; APPLICANT: Kishimoto, Uiro  
; APPLICANT: Nishiyama, Toshio  
; APPLICANT: Ehama, Ritsuko  
; TITLE OF INVENTION: METHODS FOR EVALUATING A COMPOUND FOR  
; TITLE OF INVENTION: ITS EFFECT ON SKIN  
; FILE REFERENCE: 10287-054001  
; CURRENT APPLICATION NUMBER: US/09/393,483A  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: 09/070,436  
; PRIOR FILING DATE: 1998-04-30  
; PRIOR APPLICATION NUMBER: 60/069,945  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 5069  
; TYPE: DNA

ORGANISM: Homo sapiens  
US-09-393-483A-1  
Query Match 29.7%; Score 1569.8; DB 3; Length 5069;  
Best Local Similarity 86.3%; Pred. No. 0;  
Matches 1847; Conservative 0; Mismatches 112; Indels 180; Gaps 3;  
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Db AAAGCGCAAAAGGCGAGAAACCGTAAAGGCGCGGCTTGTGCGGTTTTCATAGG 4946  
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Db ACAGAGCTATTAAGATACGAGGCGTTTCCCGTGAAGCTCCCTGCGCTCCGTT 4826  
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Db CCGACCCCTGCGCTTACCGGATACCTGTCCGCTTTCTCCCTTGGGAAAGCTGGCCTT 4766  
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Db TGTGTGACGAAACCCCGCTCAGCCGACCGCTGCGCTTATCCGGTATATCGTCTT 4646  
Qy GAGTCCAAACCGGTATAGACACGACTTATCCGACATGGCAGACGACATGTGAA 3492  
Db GAGTCCAAACCGGTATAGACACGACTTATCCGACATGGCAGACGACATGTGAA 4586  
Qy AGCAGAGGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGTGCTTAACTAG 3552  
Db AGCAGAGGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGTGCTTAACTAG 4526  
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Qy TCGTCGACCAAGCGGCATGTGCTT----- 3819  
Db TCGTCGACCAAGCGGCATGTGCTT----- 4226  
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Qy GATGCGCGATAGCGCTGTGTTTCTGTATGCGGATTTGCACTGCGG----- 3900  
Db GATGCGCGATAGCGCTGTGTTTCTGTATGCGGATTTGCACTGCGG----- 4166  
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Db CCTGGGCTTCACTCGGAACTTGGGGGCTGGGGTGGGAAAGAAAGAAAGCGGCGAT 3901  
Qy TGAACCTCGCGAGGTGCTGTCAGCTCAGGCAAGCACTGAACCAACTGCGG 3951  
Db TGAACCTCGCGAGGTGCTGTCAGCTCAGGCAAGCACTGAACCAACTGCGG 3951

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Qy AGGGATGCA----- 3961  
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Qy -----GCCCGGGTGG 3972  
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Db TGTCTGATAGCGGTCCGACACCCAGCGCGCAAGTCGATGAATCCAGAAAACGCG 3506  
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Db GCAATTCATTCAGAGGACCCGACAGGTGCTTGAACAAAAGAACCGGCGCTGCG 4872  
Qy CTGACAGCGGAAACAGCGCGCATTCAGAGACGCGATTTGTGTGCCATCATAGC 4872  
Db CTGACAGCGGAAACAGCGCGCATTCAGAGACGCGATTTGTGTGCCATCATAGC 3026  
Qy CGAATGCGCTCTCCACACCGGCGGAGAACTGCGTGCATTCATCTTGTTCATCA 4932  
Db CGAATGCGCTCTCCACACCGGCGGAGAACTGCGTGCATTCATCTTGTTCATCA 2966

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QY	4933	TGCGAAGATCTCATCTGTCTTGGATAGATCTTG	4971
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Search completed: May 14, 2006, 02:24:57  
Job time : 654 secs

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Db 361 GCAACAGACGGGTCTTAACAGGATTTGACGAACTGAATTCGCATTTGACAGATATT 420  
Qy 421 GTATTTAAGTCCAGAGCTCGATACAAATAAGCCATTGTGACATTCGCAATGAGTGTG 480  
Db 421 GTATTTAAGTCCAGAGCTCGATACAAATAAGCCATTGTGACATTCGCAATGAGTGTG 480  
Qy 481 CACCTGGGTTGGAGTCGATCATCATGCACTCGTGGGCTTCTTCTGTGTGGCGTGTCT 540  
Db 481 CACCTGGGTTGGAGTCGATCATCATGCACTCGTGGGCTTCTTCTGTGTGGCGTGTCT 540  
Qy 541 CTGCTGCCCTGGCTGTCTCCGGGTCTCTGCGAAGGCGCCGGCCGGCCGGCCCTTC 600  
Db 541 CTGCTGCCCTGGCTGTCTCCGGGTCTCTGCGAAGGCGCCGGCCGGCCGGCCCTTC 600  
Qy 601 GAGTCCGGACTCGACCTCTGCGAAGCGGAGCCGAGCGGGTGAAGCCAGGCTTATGCA 660  
Db 601 GAGTCCGGACTCGACCTCTGCGAAGCGGAGCCGAGCGGGTGAAGCCAGGCTTATGCA 660  
Qy 661 AGCAAAATCTGAGAGGAGGATTACGGTCTGTGTCAAGTGAATGAATCATGACTGTA 720  
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Db 841 CATTTAATAACAAGATCTTGAAGAAATGATTGATATGATGAGAGAAAGACTCAATGATG 900  
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Qy 1861 TCTTCTACACACCATATGCCCGCGGAAAGTGAAGACCAACAAGGTAAGCTGTCTCT 1920  
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Db 2041 AGCAATATGTAAACATGTAGCTGACAGGAGAGTGAAGATCTTCTTAATCTCTA 2100  
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Qy 2281 TAAAGTGAAGAAAGCTGTGCTAATCAGGGGTGCTCAGCTCTCTTAATCTGATGT 2340  
Db 2281 TAAAGTGAAGAAAGCTGTGCTAATCAGGGGTGCTCAGCTCTCTTAATCTGATGT 2340  
Qy 2341 CCAATGATCTTTGCTTCTGTGTGCTGATGCTGACCTGCTGCTGATGATGATGATGAT 2400  
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Db 2401 GCAAGTGGCAACAATGAGCTGAGTGAAGGCCCGGGGGAGTGAACCTTGAACCTTGGCA 2460  
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Db 2461 CTGAGGTGGCCCGGCAAGAGCGGCTGATGATGATGATGATGATGATGATGATGATGAT 2520

QY	2521	CTCTACCAACTGAGAACTACTGCAACTAGGCCCACTACACTCTGTCCACCCTCTGCA	2580
Db	2521	CTCTACCAACTGAGAACTACTGCAACTAGGCCCACTACACTCTGTCCACCCTCTGCA	2580
QY	2581	ATGAATPAAAACCTTGAAAGAGCACTACAAGTTGTGTATACATGAGTGCATGTGCATATG	2640
Db	2581	ATGAATPAAAACCTTGAAAGAGCACTACAAGTTGTGTATACATGAGTGCATGTGCATATG	2640
QY	2641	TGTCGCGGGGGGACATGAGTGGGCTGACTGAGTGGTCGGGCTTATCTATCTGGCA	2700
Db	2641	TGTCGCGGGGGGACATGAGTGGGCTGACTGAGTGGTCGGGCTTATCTATCTGGCA	2700
QY	2701	GCTGTCTAGACSTAACTCATGTCTCATAGCTGTTTCTGTGTGAATTTGTTATCCGCTCA	2760
Db	2701	GCTGTCTAGACSTAACTCATGTCTCATAGCTGTTTCTGTGTGAATTTGTTATCCGCTCA	2760
QY	2761	ATTCCACAACAATACATACGAGCGGGAGCACTAAAGTGTAAAGCTGGGGGCTTAATGANTG	2820
Db	2761	ATTCCACAACAATACATACGAGCGGGAGCACTAAAGTGTAAAGCTGGGGGCTTAATGANTG	2820
QY	2821	AGCTAACTCACATTAAATTGGCTTGGGCTCACTGCGCGCTTTTCAAGTCGGGAAACCTGTG	2880
Db	2821	AGCTAACTCACATTAAATTGGCTTGGGCTCACTGCGCGCTTTTCAAGTCGGGAAACCTGTG	2880
QY	2881	TGCCAGCTGCATTAAATGAATCGGTCGAACCGCGGGGAGAGGCGGTTTGCATATTGGGCGC	2940
Db	2881	TGCCAGCTGCATTAAATGAATCGGTCGAACCGCGGGGAGAGGCGGTTTGCATATTGGGCGC	2940
QY	2941	TCTTCGCGTTTCTCGCTCACTGACCTCGCTGGGCTGTGGCTGTTCGGCTGCGGCGAGCGGTA	3000
Db	2941	TCTTCGCGTTTCTCGCTCACTGACCTCGCTGGGCTGTGGCTGTTCGGCTGCGGCGAGCGGTA	3000
QY	3001	TCAGCTCACTCAAAGGCGGTAAATACGTTATTCACAGAAATACAGGGGATPAAACGAGAAAG	3060
Db	3001	TCAGCTCACTCAAAGGCGGTAAATACGTTATTCACAGAAATACAGGGGATPAAACGAGAAAG	3060
QY	3061	AACATGTAGCAAAAAGGCGCAGCAAAAAGGCGAGAAACCGTAAAAAGGCGCGCTTCTGGCG	3120
Db	3061	AACATGTAGCAAAAAGGCGCAGCAAAAAGGCGAGAAACCGTAAAAAGGCGCGCTTCTGGCG	3120
QY	3121	TTTTTCCATAAGCTTCGCGCCCCCTTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGG	3180
Db	3121	TTTTTCCATAAGCTTCGCGCCCCCTTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGG	3180
QY	3181	TGGCGAAAACCGGACGAGACTPAAAAGATPACAGAGGGTTTCCCGCGGAGAGTCCCTCGTG	3240
Db	3181	TGGCGAAAACCGGACGAGACTPAAAAGATPACAGAGGGTTTCCCGCGGAGAGTCCCTCGTG	3240
QY	3241	CGCTCTCTGTTCGCAACCCCTGACCGGTTACCGGATACCTGTCGCGCTTCTCCCTCGGGA	3300
Db	3241	CGCTCTCTGTTCGCAACCCCTGACCGGTTACCGGATACCTGTCGCGCTTCTCCCTCGGGA	3300
QY	3301	AGCGTGGGCTTTCTCATAGCTCAACGCTGTAGGTATCTCAAGTTGCGGTATAGTGTGCTCGC	3360
Db	3301	AGCGTGGGCTTTCTCATAGCTCAACGCTGTAGGTATCTCAAGTTGCGGTATAGTGTGCTCGC	3360
QY	3361	TCGAAGCTGGGCTGTGTGACGAAACCCCGGTTACGCGGACCGGTCGCGCTTATCCGGT	3420
Db	3361	TCGAAGCTGGGCTGTGTGACGAAACCCCGGTTACGCGGACCGGTCGCGCTTATCCGGT	3420
QY	3421	AACATATGCTTTTGAAGTCCAACCCGGTAAAGACACGACTTATGCGCATGTGGCAGCGCACT	3480
Db	3421	AACATATGCTTTTGAAGTCCAACCCGGTAAAGACACGACTTATGCGCATGTGGCAGCGCACT	3480
QY	3481	GCTAACAGGATTTAGCAGCGGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGTGG	3540
Db	3481	GCTAACAGGATTTAGCAGCGGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGTGG	3540
QY	3541	CCTAACCTACGGCTACACTPAGAAAGAACGTAATTTGGTATCTGCGCTCTGCTGAAACCGATT	3600
Db	3541	CCTAACCTACGGCTACACTPAGAAAGAACGTAATTTGGTATCTGCGCTCTGCTGAAACCGATT	3600
QY	3601	ACCTTCGAAAAGATTGTAGCTCTTGATCTCGGCAAAACAACCGCTGTAGTGGGT	3660

Dp	3601	ACCTTCGGAAGAAAGATTGGTAGCTCTTGATCCGGCAACAAACCAACCGCTGGTAGCGGT	3660
Oy	3661	GGTTTTTTTGTGGAAGACAGATTACGGGACGAGAAAAAAGATCTCAAGANAATCT	3722
Dp	3661	GGTTTTTTTGTGGAAGACAGATTACGGGACGAGAAAAAAGATCTCAAGANAATCT	3722
Oy	3721	TTGATCTTTTCTACGGGGTCTGACCCCTCAGTGAACGAAAACTCAGTTAAGGATTTTG	3780
Dp	3721	TTGATCTTTTCTACGGGGTCTGACCCCTCAGTGAACGAAAACTCAGTTAAGGATTTTG	3780
Oy	3781	GTCAAGAGATTATCGTGCACCAAGCGGCATCGTGCTCCCACTCTCGAGTTGCGGG	3840
Dp	3781	GTCAAGAGATTATCGTGCACCAAGCGGCATCGTGCTCCCACTCTCGAGTTGCGGG	3840
Oy	3841	GGATGGAAGCGCGGATACCGCGCTGTGGTTTCTCGAATGCCGACGATTTTGCATGCGCG	3900
Dp	3841	GGATGGAAGCGCGGATACCGCGCTGTGGTTTCTCGAATGCCGACGATTTTGCATGCGCG	3900
Oy	3901	TAGAATCTCCGCGAGGTCTGCAGCCTCAGGACAGCTGAAACCAACTCGCAGGGGATCG	3960
Dp	3901	TAGAATCTCCGCGAGGTCTGCAGCCTCAGGACAGCTGAAACCAACTCGCAGGGGATCG	3960
Oy	3961	AGCCCGGGGTGGGCGAAGAACTCCAGCATGAGATCCCGCGCTGAGGATCATCCAGCG	4020
Dp	3961	AGCCCGGGGTGGGCGAAGAACTCCAGCATGAGATCCCGCGCTGAGGATCATCCAGCG	4020
Oy	4021	GGTCTCCGGAAGAAAGATTTCCGAAGCCCACTTTTCATATGAAGGCGCGGTGAATCGAA	4080
Dp	4021	GGTCTCCGGAAGAAAGATTTCCGAAGCCCACTTTTCATATGAAGGCGCGGTGAATCGAA	4080
Oy	4081	TCTCGTAGTAGCAGGTTGGGGGTGCGTTGATCGGTCAATTGAAACCCAGAGTCCCGCTC	4140
Dp	4081	TCTCGTAGTAGCAGGTTGGGGGTGCGTTGATCGGTCAATTGAAACCCAGAGTCCCGCTC	4140
Oy	4141	AGAAGAACTCGTCAAGAAAGCGGATGAAAGCGATGCGCTGCGAATCGGAGCGGCGATAC	4200
Dp	4141	AGAAGAACTCGTCAAGAAAGCGGATGAAAGCGGATGCGCTGCGAATCGGAGCGGCGATAC	4200
Oy	4201	CGTAAAGACAGAGAAAGGAGTCAAGCCATTTGGCGCCCAAGCTTTTCAGCAATATCACGG	4260
Dp	4201	CGTAAAGACAGAGAAAGGAGTCAAGCCATTTGGCGCCCAAGCTTTTCAGCAATATCACGG	4260
Oy	4261	TAGCCAAACGATGATGCTGATAGGGGTCCGCAACCCAGCGCGCACAGTCGATGAATC	4320
Dp	4261	TAGCCAAACGATGATGCTGATAGGGGTCCGCAACCCAGCGCGCACAGTCGATGAATC	4320
Oy	4321	CAGAAAGCGGCATTTTTCACATGATATTCCGCAAGCAGGCAATCGCATGGGTCACGA	4380
Dp	4321	CAGAAAGCGGCATTTTTCACATGATATTCCGCAAGCAGGCAATCGCATGGGTCACGA	4380
Oy	4381	CGAGATCTCGCCGTCCGGGCATGCGCGCTTGGAACCTGGCCCAAGTTCCGCTGGCGGA	4440
Dp	4381	CGAGATCTCGCCGTCCGGGCATGCGCGCTTGGAACCTGGCCCAAGTTCCGCTGGCGGA	4440
Oy	4441	GGCCCTGATGCTCTTCCGTCAGATCATCTCGAATGCAAGACGCGGCTTTCATCCGAGTAC	4500
Dp	4441	GGCCCTGATGCTCTTCCGTCAGATCATCTCGAATGCAAGACGCGGCTTTCATCCGAGTAC	4500
Oy	4501	GTGCTCGCTCATGCGATGTTTCGCTTGATGATGGAATGGGACAGTATGCGCATCAAGC	4560
Dp	4501	GTGCTCGCTCATGCGATGTTTCGCTTGATGATGGAATGGGACAGTATGCGCATCAAGC	4560
Oy	4561	TATGACGCGCGCGCATTTGCATCAACCCATGATGATATCTTCTCGGACGAGCAAGTGAG	4620
Dp	4561	TATGACGCGCGCGCATTTGCATCAACCCATGATGATATCTTCTCGGACGAGCAAGTGAG	4620
Oy	4621	ATGACAGAGATCTGCGCCCGGACCTTGCCCAATACAGCAAGTCCCTTCCGCTTACG	4680
Dp	4621	ATGACAGAGATCTGCGCCCGGACCTTGCCCAATACAGCAAGTCCCTTCCGCTTACG	4680
Oy	4681	TGAACAGTCGACGACAGCTGCGCAAGAAACGCTCGTGGCCAGCACGATAGCCGCG	4740



Db	4681	TGACACAGCTGAGACACAGCTGCGCAGAGAAAGCCCGCTGCGGCAACCAAGATAGCCGGG	4740
Qy	4741	CTGCGCTGCTCTGCAAGTTCAATTCAGGGCAACGGACAGGTCGGTCTTGACAAAAGAACCG	4800
Db	4741	CTGCGCTGCTCTGCAAGTTCAATTCAGGGCAACGGACAGGTCGGTCTTGACAAAAGAACCG	4800
Qy	4801	GGGGCCCCCTGGCGTGAACGCGCGGAAACACGCGCGGATCAGAGCAGCCGATGTCGTGTTG	4860
Db	4801	GGGGCCCCCTGGCGTGAACGCGCGGAAACACGCGCGGATCAGAGCAGCCGATGTCGTGTTG	4860
Qy	4861	CCAGTCATAGCCGAATAGCCTCTCCACCCAGCGCGCGAGAACTTGCCTGCAATTCAT	4920
Db	4861	CCAGTCATAGCCGAATAGCCTCTCCACCCAGCGCGCGAGAACTTGCCTGCAATTCAT	4920
Qy	4921	CTTGTTATATCATAGCCAAACGATCTCTCATCTGTCCTTGATCAGATCTTGATCCCTGC	4980
Db	4921	CTTGTTATATCATAGCCAAACGATCTCTCATCTGTCCTTGATCAGATCTTGATCCCTGC	4980
Qy	4981	GCCATCAGATCTCTGGCGGCAAGAAACCATCCAGTTACTTTGACAGGCGCTCCCAACT	5040
Db	4981	GCCATCAGATCTCTGGCGGCAAGAAACCATCCAGTTACTTTGACAGGCGCTCCCAACT	5040
Qy	5041	TACCAAGAGGCGCCCAAGCTGGCAATTCGGGTTGCTTGGCTGCTATATAACCGCCCAAT	5100
Db	5041	TACCAAGAGGCGCCCAAGCTGGCAATTCGGGTTGCTTGGCTGCTATATAACCGCCCAAT	5100
Qy	5101	CTAGCTTATCGCATATGTAAGCCCACTGCAAGCTACCTGTTTCCTTGGCGCTTGCCTTT	5160
Db	5101	CTAGCTTATCGCATATGTAAGCCCACTGCAAGCTACCTGTTTCCTTGGCGCTTGCCTTT	5160
Qy	5161	CCCTTGTTCAGATAGCCCAAGTAGCTGACATTCATCGGCGGTCAAGACCGTTTCTGGCGAC	5220
Db	5161	CCCTTGTTCAGATAGCCCAAGTAGCTGACATTCATCGGCGGTCAAGACCGTTTCTGGCGAC	5220
Qy	5221	TGGCTTTTCTAGAGTTCGCTTCCTTTAGCAGCCCTTGCGCCGAGTGTGCGGAGC	5280
Db	5221	TGGCTTTTCTAGAGTTCGCTTCCTTTAGCAGCCCTTGCGCCGAGTGTGCGGAGC	5280
Qy	5281	GTG 5283	
Db	5281	GTG 5283	

RESULT 2

US-10-198-478-16

; Sequence 16, Application US/10198478

; Publication No. US20030188336A1

; GENERAL INFORMATION:

APPLICANT: Corbin, David R.

APPLICANT: Romano, Charles P.

TITLE OF INVENTION: Improved Methods for Transforming Plants to Express delta-Endotoxin

FILE REFERENCE: 38-21 (13547) B

CURRENT APPLICATION NUMBER: US/10/198,478

CURRENT FILING DATE: 2002-11-12

PRIOR APPLICATION NUMBER: 09/186, 002

PRIOR FILING DATE: 1998-11-04

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PatentIn version 3.1

SEQ ID NO 16

LENGTH: 8349

TYPE: DNA

ORGANISM: artificial sequence

FEATURE: OTHER INFORMATION: completely synthesized

FEATURE: NAME/KEY: misc\_feature

LOCATION: (1) .. (8349)

OTHER INFORMATION:

US-10-198-478-16

Query Match 42.4%; Score 2240; DB 6; Length 8349;

Best Local Similarity 93.4%; Pred. No. 0;

Matches 2409; Conservative 0; Mismatches 25; Indels 144; Gaps 1;

QY	2706	CTAGACGTATTCATNGTCAGACAGCTGTTTCTGTGTGAATTTGTTATCCGCTGCACATTC	2765
Db	5911	CTTGGCGTAAATCAATGTCATAGCGTGTCTGTGTGAATTTGTTATCCGCTGCACATTC	5970
QY	2766	ACACACATTCAGAGCCGGAGACATAAAGTGTAAAGCTGGGGTGCTTAATGATGAGCTA	2825
Db	5971	ACACACATTCAGAGCCGGAGACATAAAGTGTAAAGCTGGGGTGCTTAATGATGAGCTA	6030
QY	2826	ACTCACATTAATGCGTTGGGCTCACCTGCCGCTTCCATCGGGAAACCTGTGAGCCA	2885
Db	6031	ACTCACATTAATGCGTTGGGCTCACCTGCCGCTTCCATCGGGAAACCTGTGAGCCA	6090
QY	2886	GCTGCATTAAATGAAATCGGCCAACCGCGGGGAGAGGGCGTTTGCGTAATGGGCGCTCTTC	2945
Db	6091	GCTGCATTAAATGAAATCGGCCAACCGCGGGGAGAGGGCGTTTGCGTAATGGGCGCTCTTC	6150
QY	2946	CGCTTCTCGCTCACTGACTCGCTGCGCTCGTGCTTCCGCTGGCGGAGCGTATCAGC	3005
Db	6151	CGCTTCTCGCTCACTGACTCGCTGCGCTCGTGCTTCCGCTGGCGGAGCGTATCAGC	6210
QY	3006	TCACATCAAGCGGGTAATACGGTTATCCACAGATCAGGGAGATPACGACGAAAGAACAT	3065
Db	6211	TCACATCAAGCGGGTAATACGGTTATCCACAGATCAGGGAGATPACGACGAAAGAACAT	6270
QY	3066	GTGAGCAAAAAGGCCAGACAAAAGGCCAGAGAAACCGTAAAAAAGCCGCTGTGCGTTTTT	3125
Db	6271	GTGAGCAAAAAGGCCAGACAAAAGGCCAGAGAAACCGTAAAAAAGCCGCTGTGCGTTTTT	6330
QY	3126	CCATAGGCTCTCGCCCGCTGCACAGAGCATCACAAAAATCGACGCTCAAGTACAGAGTGGCG	3185
Db	6331	CCATAGGCTCTCGCCCGCTGCACAGAGCATCACAAAAATCGACGCTCAAGTACAGAGTGGCG	6390
QY	3186	AAACCCGACAGAGCATTAATGAATATCCAGAGCGTTTCCCTCTGGAAGCTCCCTCGTGCCTC	3245
Db	6391	AAACCCGACAGAGCATTAATGAATATCCAGAGCGTTTCCCTCTGGAAGCTCCCTCGTGCCTC	6450
QY	3246	TCCTGTTCGACCCCTGCGCTTACCCGATACCTGTCCGCTTTTCCCTTGGGAAACGCT	3305
Db	6451	TCCTGTTCGACCCCTGCGCTTACCCGATACCTGTCCGCTTTTCCCTTGGGAAACGCT	6510
QY	3306	GCGCGTTTCTCATAGCTACAGCTGTAGAGGTATCTCAGTTCCGTTGAGGTCGCTCCAA	3365
Db	6511	GCGCGTTTCTCATAGCTACAGCTGTAGAGGTATCTCAGTTCCGTTGAGGTCGCTCCAA	6570
QY	3366	GCTGGGCTGTGTGACGAAACCCCGCTTACGCCCGGACCGCTGCGCTTATTCGGTAACTA	3425
Db	6571	GCTGGGCTGTGTGACGAAACCCCGCTTACGCCCGGACCGCTGCGCTTATTCGGTAACTA	6630
QY	3426	TCGTTTGAATTCMAACCCCGGTAAACANCAATTAATCCGCACTGGCAGAGCACTGGTAA	3485
Db	6631	TCGTTTGAATTCMAACCCCGGTAAACANCAATTAATCCGCACTGGCAGAGCACTGGTAA	6690
QY	3486	CAGATTTAGCAGAGGAGTATGTATAGCGGTGTACAGAGTTCTTGAAGTGTGGCCTAA	3545
Db	6691	CAGATTTAGCAGAGGAGTATGTATAGCGGTGTACAGAGTTCTTGAAGTGTGGCCTAA	6750
QY	3546	CTACGGCTACACTAGAAACAAGTATTTGGTATCTGCGCTTCTGCTGAAGCCAGTTACTT	3605
Db	6751	CTACGGCTACACTAGAAACAAGTATTTGGTATCTGCGCTTCTGCTGAAGCCAGTTACTT	6810
QY	3606	CGGAAAAAGATGGTAGCTCTGTATCCGGAAAAAACAACCAACCGCTGGTACCGGTGTTT	3665
Db	6811	CGGAAAAAGATGGTAGCTCTGTATCCGGAAAAAACAACCAACCGCTGGTACCGGTGTTT	6870
QY	3666	TTTTTGTTCAGACGACGATTAACGCGCAGAAAAAAAAGGATCTCAGAGAGATCCTTGTAT	3725
Db	6871	TTTTTGTTCAGACGACGATTAACGCGCAGAAAAAAAAGGATCTCAGAGAGATCCTTGTAT	6930
QY	3726	CTTTTCTACGGGCTCTGACGCTCAATGGAACGAAACCTCAGGTTAAGGATTTTGGTCAT	3785
Db	6931	CTTTTCTACGGGCTCTGACGCTCAATGGAACGAAACCTCAGGTTAAGGATTTTGGTCAT	6990

QY 3786 GAGATTATCTGACCAAGCGCCATGCGCTCCCACTCTCGAGTTGCGGGCANG 3845  
 Db 6991 GAGATTATCAAAAAGGATCTTCACTAGATCTT----- 7024  
 QY 3846 GATGGCGGATAGCGCGCTGCTGTTTCTTGATGCGGACGAGATTGCACTGCCGGTAGAA 3905  
 Db 7025 ----- 7024  
 QY 3906 CTCCCGAGAGTCTGCAAGCTTCAGGACAGCTGAACCAACTCGGAGGGAGTCGAGCCC 3965  
 Db 7025 -----TT 7026  
 QY 3966 GGGGTGGCGAAAGAACTCCAGCATGAGATCCCGCGCTGAGAGATCATCCAGCCGCGTC 4025  
 Db 7027 GGGGTGGCGAAAGAACTCCAGCATGAGATCCCGCGCTGAGAGATCATCCAGCCGCGTC 7086  
 QY 4026 CCGGAAAAGATTCGGAAGCCCACTTTGATGAAAGCGCGGTGGGAAATCGAAATCTTCG 4085  
 Db 7087 CCGGAAAAGATTCGGAAGCCCACTTTGATGAAAGCGCGGTGGGAAATCGAAATCTTCG 7146  
 QY 4086 TGATGGCAGTTGGCGCTCGCTTGGTGGTCAATTTGAAACCCAGAGTCCGCTCAGAG 4145  
 Db 7147 TGATGGCAGTTGGCGCTCGCTTGGTGGTCAATTTGAAACCCAGAGTCCGCTCAGAG 7206  
 QY 4146 AACTGTCAAGAAAGCGATAGAAAGCGATGCGCTGCGAATCGGAGCGCGCATACCTGAA 4205  
 Db 7207 AACTGTCAAGAAAGCGATAGAAAGCGATGCGCTGCGAATCGGAGCGCGCATACCTGAA 7266  
 QY 4206 AGCAGAGAGAAAGCGGTGACCCCATTTGCGCGCCAGACTCTTACAGAAATACAGGGTAGCC 4265  
 Db 7267 AGCAGAGAGAAAGCGGTGACCCCATTTGCGCGCCAGACTCTTACAGAAATACAGGGTAGCC 7326  
 QY 4266 AACGCTATGCTCTGATAGCGGTGCGGCAACCGCCGCGCAACATCGATGAAATCCAGAA 4325  
 Db 7327 AACGCTATGCTCTGATAGCGGTGCGGCAACCGCCGCGCAACATCGATGAAATCCAGAA 7386  
 QY 4326 AAGCGGCAATTTTCCACATGATATTTCCGCAAGCAGCATGCCATGGGTCAACAGAGA 4385  
 Db 7387 AAGCGGCAATTTTCCACATGATATTTCCGCAAGCAGCATGCCATGGGTCAACAGAGA 7446  
 QY 4386 TCTCTGCGGTGGGCAATGCGGCTTTGAGCCTGCGGAAAGTTGCGGTGCGCGAGCCCC 4445  
 Db 7447 TCTCTGCGGTGGGCAATGCGGCTTTGAGCCTGCGGAAAGTTGCGGTGCGCGAGCCCC 7506  
 QY 4446 TGATGCTCTTGTGCGATGATCTGATGCGAAGAGCGGCTTCCATCCGATAGTGTCT 4505  
 Db 7507 TGATGCTCTTGTGCGATGATCTGATGCGAAGAGCGGCTTCCATCCGATAGTGTCT 7566  
 QY 4506 CGCTCGATGCGATGTTTGTGTTGGTGTGCAATGGGCGAGTAGCGGATCAAGCGTATGC 4565  
 Db 7567 CGCTCGATGCGATGTTTGTGTTGGTGTGCAATGGGCGAGTAGCGGATCAAGCGTATGC 7626  
 QY 4566 AGCCGCGCATTTGATGATGCGCATGATGATGATCTTTCTGCGAGAGCAAGGTGATGATGAC 4625  
 Db 7627 AGCCGCGCATTTGATGATGCGCATGATGATGATCTTTCTGCGAGAGCAAGGTGATGATGAC 7686  
 QY 4626 AGGAGATCTGCGCCCGGCACTTCCGCAATAGCAGCGCATCTTCCGCTTCACTAGTACA 4685  
 Db 7687 AGGAGATCTGCGCCCGGCACTTCCGCAATAGCAGCGCATCTTCCGCTTCACTAGTACA 7746  
 QY 4686 ACCTGAGCAGAGCTGGCGAAGAACCGCTGCTGCGCAAGCAGTAGCGGAGCTGCC 4745  
 Db 7747 ACCTGAGCAGCAGCTGGCGAAGAACCGCTGCTGCGCAAGCAGTAGCGGAGCTGCC 7806  
 QY 4746 TCGTCTGCAAGTTATTCAGGAGCAACCGGACAGGTGCTTTGACAAAAGAACCGGCGC 4805  
 Db 7807 TCGTCTGCAAGTTATTCAGGAGCAACCGGACAGGTGCTTTGACAAAAGAACCGGCGC 7866  
 QY 4806 CCGTGGCGTGAACAGCGGGAACAGCGCGGCAATCAGAGCAGCGAGTTGTTGTGCGCCAG 4865  
 Db 7867 CCGTGGCGTGAACAGCGGGAACAGCGCGGCAATCAGAGCAGCGAGTTGTTGTGCGCCAG 7926  
 QY 4866 TCATAGCCGAATAGCTCTTCCACCCAGCGGCGGAGAACCTGCGTGCATTCATCTTGT 4925

Db 7927 TCATAGCCGAATAGCTCTTCCACCCAGCGGCGGAGAACCTGCGTGCATTCATCTTGT 7986  
 QY 4926 TCATATGATCGGAACAGATCTCATATCTGTCTTGTATGATGATCTTATCTTGTGCGCAT 4985  
 Db 7987 TCATATGATCGGAACAGATCTCATATCTGTCTTGTATGATGATCTTATCTTGTGCGCAT 8046  
 QY 4986 CAGATCTTGGCGGGAAGAAAGCCATTCAGATTACTTTGCAAGGCTTCCCACTTACCA 5045  
 Db 8047 CAGATCTTGGCGGGAAGAAAGCCATTCAGATTACTTTGCAAGGCTTCCCACTTACCA 8106  
 QY 5046 GAGGCGCGCCAGCTGCAATTCGCTTCCGTTGCTGTCATTAATAACGCGCAGCTAGC 5105  
 Db 8107 GAGGCGCGCCAGCTGCAATTCGCTTCCGTTGCTGTCATTAATAACGCGCAGCTAGC 8166  
 QY 5106 TATGCGCATGTAAGCCCATGCAAGCTACTGCTTTCTTTGCGCTTCCCTT 5165  
 Db 8167 TATGCGCATGTAAGCCCATGCAAGCTACTGCTTTCTTTGCGCTTCCCTT 8226  
 QY 5166 GTCCAGATAGCCCATGATGCTGATTCATTCGCGGTGACACCGTTTCTGCGAGATGCT 5225  
 Db 8227 GTCCAGATAGCCCATGATGCTGATTCATTCGCGGTGACACCGTTTCTGCGAGATGCT 8286  
 QY 5226 TTCTACGTTTCCGCTTCTTTAGCAGCGCTTGGCGCCTGAGTGTTCGCGAGGCTG 5283  
 Db 8287 TTCTACGTTTCCGCTTCTTTAGCAGCGCTTGGCGCCTGAGTGTTCGCGAGGCTG 8344

RESULT 3  
 US-10-841-796-33  
 ; Sequence 33, Application US/10841796  
 ; Publication No. US20040237138A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Monsanto Biotechnology Corporation  
 ; APPLICANT: Monsanto Technology LLC  
 ; APPLICANT: Nordine, Chiekh  
 ; APPLICANT: Fisher, Dane  
 ; APPLICANT: Thompson, Rebecca  
 ; TITLE OF INVENTION: A method of increasing yield in a plant  
 ; FILE REFERENCE: Docket number 38-21 (15691)B  
 ; CURRENT FILING DATE: 2004-07-05  
 ; NUMBER OF SEQ ID NOS: 34  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 33  
 ; LENGTH: 11546  
 ; TYPE: DNA  
 ; ORGANISM: Artificial  
 ; FEATURE:  
 ; OTHER INFORMATION: plasmid containing construct for corn transformation  
 US-10-841-796-33

Query Match 42.4%; Score 2240; DB 8; Length 11546;  
 Best Local Similarity 93.4%; Pred. No. 0;  
 Matches 2409; Conservative 0; Mismatches 25; Indels 144; Gaps 1;  
 QY 2706 CTAGAGTATCATGCTGATGATGCTGTTCTGTGTGAATTTGATTCGCTCACAATTCC 2765  
 Db 9108 CTGGCGCTTAATCATGCTGATGATGCTGTTCTGTGTGAATTTGATTCGCTCACAATTCC 9167  
 QY 2766 ACACAATCATGAGCGGGAAGCATTAAGTGTAAAGCCTGGGGTGCCTAAAGAGAGCTA 2825  
 Db 9168 ACACAATCATGAGCGGGAAGCATTAAGTGTAAAGCCTGGGGTGCCTAAAGAGAGCTA 9227  
 QY 2826 ACTCATTAATTTGCTGTTGCTCATCTGCCGCTTTCCAGTGGGAAACCTGTGCTGCA 2885  
 Db 9228 ACTCATTAATTTGCTGTTGCTCATCTGCCGCTTTCCAGTGGGAAACCTGTGCTGCA 9287  
 QY 2886 GCTGCATTAATGATTCGCGCAAGCGCGGGAAGAGCGGTTTGCGTAAATTTGCGCTCTTC 2945  
 Db 9288 GCTGCATTAATGATTCGCGCAAGCGCGGGAAGAGCGGTTTGCGTAAATTTGCGCTCTTC 9347  
 QY 2946 CGCTTCTGCTCACTGACTCGCTGCGCTGCTGCTTCCGCTGCGGAGCGGATGACG 3005

[illegible]

Db	10284	CCGGAATAACAATTCCGAAGCCCAACTTTTCAATGAAAGCGCGGTGGAAATGAAATCTGC	10343
OY	4086	TGATGGACGGTTGGGCGTGCCTTGGTGGGTCAATTTGAAACCCAGAGTCCCGCTCAAGAA	4145
Db	10344	TGATGGACGGTTGGGCGTGCCTTGGTGGGTCAATTTGAAACCCAGAGTCCCGCTCAAGAG	10403
OY	4146	AACCTGTCAGAAAGGCGATAGAAAGCGATGGCGCTGCGAATCGGAGACGGCCATACCTTAA	4205
Db	10404	AACCTGTCAGAAAGGCGATAGAAAGCGATGGCGCTGCGAATCGGAGACGGCCATACCTTAA	10463
OY	4206	AGCAGAGGAAGCGGTCAAGCCATTTGCGCGCAAGCTTTTCAGCATATTCACGGGTAGCC	4265
Db	10464	AGCAGAGGAAGCGGTCAAGCCATTTGCGCGCAAGCTTTTCAGCATATTCACGGGTAGCC	10523
OY	4266	AACGCTATGTCCTATTAAGCGGTCCGCCACACCGACGGCGCCACAGTCGATTAATTCAGAA	4325
Db	10524	AACGCTATGTCCTATTAAGCGGTCCGCCACACCGACGGCGCCACAGTCGATTAATTCAGAA	10583
OY	4326	AAGCGGCATTTTCCACCAATGATATTTCCGCAAGCAGGATGCGCATGGGTCAACGACAGA	4385
Db	10584	AAGCGGCATTTTCCACCAATGATATTTCCGCAAGCAGGATGCGCATGGGTCAACGACAGA	10643
OY	4386	TCCTTGCCTGCGGGATATCGGCGCTTGAAGCCTGGGGAACAGTTGGGCTGGCGCGACGCC	4445
Db	10644	TCCTTGCCTGCGGGATATCGGCGCTTGAAGCCTGGGGAACAGTTGGGCTGGCGCGACGCC	10703
OY	4446	TCATGCTCTTGCCTCAGATTCATCTCTGATTCGACAAACCGGCTTTCATTCGAGTACGTGCT	4505
Db	10704	TCATGCTCTTGCCTCAGATTCATCTCTGATTCGACAAACCGGCTTTCATTCGAGTACGTGCT	10763
OY	4506	CGCTGATGTCGATGTTTGGCTTGGTGTGCAATGGGACGGTATGCGGATCAAGCGTATGC	4565
Db	10764	CGCTGATGTCGATGTTTGGCTTGGTGTGCAATGGGACGGTATGCGGATCAAGCGTATGC	10823
OY	4566	AGCCGCGCATGTCATTCAGCCATGATGATTACTTTTCGGCAGAGCAAGGTGAGATGAC	4625
Db	10824	AGCCGCGCATGTCATTCAGCCATGATGATTACTTTTCGGCAGAGCAAGGTGAGATGAC	10883
OY	4626	AGGAGATCTTGCCTCCGCGCACTTTCGCCAATACAGCAGTCCCTTCCGCTCAAGTACA	4685
Db	10884	AGGAGATCTTGCCTCCGCGCACTTTCGCCAATACAGCAGTCCCTTCCGCTCAAGTACA	10943
OY	4686	ACGTGACAGACAGACTGCGCAAGGAAGCCCGTGTGTGGCCAGCCACGATATGCGCGCTGCC	4745
Db	10944	ACGTGACAGACAGACTGCGCAAGGAAGCCCGTGTGTGGCCAGCCACGATATGCGCGCTGCC	11003
OY	4746	TCGTCTCTGACATTCAATTCAGGCGCACCGGACAGTGCCTTTCGACAAAAGAAACCGGACGC	4805
Db	11004	TCGTCTCTGACATTCAATTCAGGCGCACCGGACAGTGCCTTTCGACAAAAGAAACCGGACGC	11063
OY	4806	CCCTGGCTGACAGCGCGGAACCGGCGGATTCAGACAGCCGATTTGTGTGTGCCAG	4865
Db	11064	CCCTGGCTGACAGCGCGGAACCGGCGGATTCAGACAGCCGATTTGTGTGTGCCAG	11123
OY	4866	TCATAGCCGAATAGCCTTTCACCCCAAGCGGCGGGAACCTGCGGTCATTCATCTTGT	4925
Db	11124	TCATAGCCGAATAGCCTTTCACCCCAAGCGGCGGGAACCTGCGGTCATTCATCTTGT	11183
OY	4926	TCATATATGGAAGAACATTCCTCATCCTGTCTCTTGAATCAGATCTTGAATCCCTGCGCAT	4985
Db	11184	TCATATATGGAAGAACATTCCTCATCCTGTCTCTTGAATCAGATCTTGAATCCCTGCGCAT	11243
OY	4986	CAGATCCTTGGCGGCAAGAAAGCCATTCAGTTTACTTTCAGAGGCTTCCCAACTTACCA	5045
Db	11244	CAGATCCTTGGCGGCAAGAAAGCCATTCAGTTTACTTTCAGAGGCTTCCCAACTTACCA	11303
OY	5046	GAGGGCGCCCAAGTCGACATTCGCGTTCGTTGCTCTCATATAAAACCGCCCACTTACG	5105
Db	11304	GAGGGCGCCCAAGTCGACATTCGCGTTCGTTGCTCTCATATAAAACCGCCCACTTACG	11363
OY	5106	TATGCGCATGTAAGCCCACTGCAAGCTACCTGCTTTCTCTTGGCGTTTGGCTTTCCCTT	5165
Db	11364	TATGCGCATGTAAGCCCACTGCAAGCTACCTGCTTTCTCTTGGCGTTTGGCTTTCCCTT	11423

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QY 5166 GTCCAGATAGCCCACTAGTGAATTCATCCGGGGTCAAGACCGTTTCTGCGAGTGGCT 5225
DB 11424 GTCCAGATAGCCCACTAGTGAATTCATCCGGGGTCAAGACCGTTTCTGCGAGTGGCT 11483
QY 5226 TTCTACGCTGTTCCGCTTCTTTAGACGCCCTTGCCCTGAGTGGCTGGCGAGCGTG 5283
DB 11484 TTCTACGCTGTTCCGCTTCTTTAGACGCCCTTGCCCTGAGTGGCTGGCGAGCGTG 11541

RESULT 4
US-10-322-360-1/c
; Sequence 1, Application US/10322360
; Publication No. US20030165946a1
; GENERAL INFORMATION:
; APPLICANT: Evans, Glen A.
; TITLE OF INVENTION: A Method for the Complete Chemical
; TITLE OF INVENTION: Synthesis and Assembly of Genes and Genomes
; FILE REFERENCE: P-EA 511
; CURRENT APPLICATION NUMBER: US/10/322,360
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 09/554,929
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4800
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic plasmid
US-10-322-360-1

Query Match 33.9%; Score 1793.4; DB 6; Length 4800;
Best Local Similarity 91.8%; Pred. No. 0;
Matches 1980; Conservative 0; Mismatches 1; Indels 176; Gaps 1;

QY 3127 CATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCA 3186
DB 4800 CATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCA 4741
QY 3187 AACCCGACAGGACTATTAAGATACAGGCGTTTCCCTGGAAGCTCCCTGTGGCTCT 3246
DB 4740 AACCCGACAGGACTATTAAGATACAGGCGTTTCCCTGGAAGCTCCCTGTGGCTCT 4681
QY 3247 CCTGTCGACCCCTGCGCTTACCGGATACCTGTCCGCTTTCCTTCCGGGAAGCGTG 3306
DB 4680 CCTGTCGACCCCTGCGCTTACCGGATACCTGTCCGCTTTCCTTCCGGGAAGCGTG 4621
QY 3307 GCGCTTCTCATAGCTACGCTGATGATCTCAAGTTGAGTGGTGGTGGCTTCCGCTCAAG 3366
DB 4620 GCGCTTCTCATAGCTACGCTGATGATCTCAAGTTGAGTGGTGGTGGCTTCCGCTCAAG 4561
QY 3367 CTGGGCTGTGTGCA GAACCCCGCTTCAAGCCGACCGCTGCGCTTATCCGCTACTAT 3426
DB 4560 CTGGGCTGTGTGCA GAACCCCGCTTCAAGCCGACCGCTGCGCTTATCCGCTACTAT 4501
QY 3427 CGTCTTGAATCCAAACCGGTAAAGACAGCTTATCCGCACTGGCAGACGCACTGGTAAC 3486
DB 4500 CGTCTTGAATCCAAACCGGTAAAGACAGCTTATCCGCACTGGCAGACGCACTGGTAAC 4441
QY 3487 AGATTAGCAGAGGAGTATGTAGCGGTGCTACAGAGTCTTGAAGTGGTGGCTTAAC 3546
DB 4440 AGATTAGCAGAGGAGTATGTAGCGGTGCTACAGAGTCTTGAAGTGGTGGCTTAAC 4381
QY 3547 TAGCGTACACTAAGAAAGATTTGGTATCTGCGCTGTGTAAGCCAGTTACCTTC 3606
DB 4380 TAGCGTACACTAAGAAAGATTTGGTATCTGCGCTGTGTAAGCCAGTTACCTTC 4321
QY 3607 GGAAGAAAGATTTGGTATCTTGAATCCGGCAAAACAAACACCGCTGGTGAAGGCTGTTT 3666
DB 4320 GGAAGAAAGATTTGGTATCTTGAATCCGGCAAAACAAACACCGCTGGTGAAGGCTGTTT 4261
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QY 3667 TTTGTTTCAAGCAGACAGATTACGGCGAGAAAAAAGATCTCAAGAAATCTTTGATC 3726
DB 4260 TTTGTTTCAAGCAGACAGATTACGGCGAGAAAAAAGATCTCAAGAAATCTTTGATC 4201
QY 3727 TTTTCTACGGGCTGTGACGCTCAAGTGAACGAAAACTCAAGTTAAGGATTTTGTGATG 3786
DB 4200 TTTTCTACGGGCTGTGACGCTCAAGTGAACGAAAACTCAAGTTAAGGATTTTGTGATG 4142
QY 3787 AGATTATGTGACCAAGCAAGCGCATCGTGCTCCCACTCTGTGAGTTCCGGGGCATAG 3846
DB 4141 ----- 4142
QY 3847 ATGCGGATAGCCGCTGCTGTTTCTGATGCCGACGATTTGCACTGCCGATGAAC 3906
DB 4141 ----- 4142
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DB 4141 -----GCCCG 4137
QY 3967 GGTGGGGAAGAACTCCAGATGAGATCCCGCGCTGGAGAGATCATCCAGCCGCGTCC 4026
DB 4136 GGTGGGGAAGAACTCCAGATGAGATCCCGCGCTGGAGAGATCATCCAGCCGCGTCC 4077
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DB 3956 ACTGCTCAAGAAAGCGATTAAGAGCGATGCGCTCGAATCGGAGCGCGCATTAACCTTAA 3897
QY 4207 GCAAGAAAGCGGCTGAGCCCATTCGCGCGCAAGCTCTTCAAGAAATCAAGGCTGAGCCA 4266
DB 3896 GCAAGAAAGCGGCTGAGCCCATTCGCGCGCAAGCTCTTCAAGAAATCAAGGCTGAGCCA 3837
QY 4267 AGGCTATGCTCTGATAGCGGCTCGGCAACAGCCAGCGGCGCAAGTCAATGATCAAGAA 4326
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DB 3776 AGCGGCAATTTTCCACCATGATATTTCCGCAAGCAGCATGCGCATGGGTCAAGCAGAT 3717
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DB 3716 CCTGCGGCTGCGGCAATGCGGCTTGAAGCTGAGGCAAGTTGGGCTGGGCGGAGCCCT 3657
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DB 3656 GATGCTTTGCTCCAGATCAATCTGATCGAACAGACCGGCTTCCATCCGATGATGCTC 3597
QY 4507 GCTCGATGCAATGTTTGTGCTTGGTGTGCAATGGGCAAGTACCAGTCAAGCTATGCA 4566
DB 3596 GCTCGATGCAATGTTTGTGCTTGGTGTGCAATGGGCAAGTACCAGTCAAGCTATGCA 3537
QY 4567 GCGCGGCAATGCAATGAGCATGAGATGAGTACTTCTCGGCAAGGAGCAAGGAGATGCA 4626
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QY 4627 GGAAGTCTTCCCGGCACTTCCGCAATAGCAGCGCTTCCGCTTCCGCTTCAAGTGA 4686
DB 3476 GGAAGTCTTCCCGGCACTTCCGCAATAGCAGCGCTTCCGCTTCCGCTTCAAGTGA 3417
QY 4687 GCTGAGCAAGCTGCGCAAGAAAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4746
DB 3416 GCTGAGCAAGCTGCGCAAGAAAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3357
QY 4747 GCTGCTGCAATTCATTCAGGGAACCGGACAGGTGCGTCTTGACAAAAAAGAACGGGCGCC 4806
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Db 3356 CGTCTGCAATTCATTATGAGGCAACCGGACAGTGGCTCTTGAACAAAAGAACGGGGGCC 3297  
Qy 4807 CTTGCGCTGACAGCGGGAACAGCGGCGCATCAGAGCAGCCGATTTGCTGTGTCAGT 4866  
Db 3296 CTTGCGCTGACAGCGGGAACAGCGGCGCATCAGAGCAGCCGATTTGCTGTGTCAGT 3237  
Qy 4867 CATAGCCGAATAGCTCTTCCACCCAAAGCGGCGGGAACCTGCTGTGAATTCATTTGTT 4926  
Db 3236 CATAGCCGAATAGCTCTTCCACCCAAAGCGGCGGGAACCTGCTGTGAATTCATTTGTT 3177  
Qy 4927 CAATCATGCGAAACGATCTCTCATCTCTTGTATGATAGATCTTGATCCCTGGCCATC 4986  
Db 3176 CAATCATGCGAAACGATCTCTCATCTCTTGTATGATAGATCTTGATCCCTGGCCATC 3117  
Qy 4987 AGATCTTGGCGGGAAGAAAGCCATCCAGTTTACTTTGACAGGGCTTCCAACTTACAG 5046  
Db 3116 AGATCTTGGCGGGAAGAAAGCCATCCAGTTTACTTTGACAGGGCTTCCAACTTACAG 3057  
Qy 5047 AGGGCGCCGACGCTGGGAATTCGGGTTGCTGTGTCATTAACCGCCCACTAGT 5106  
Db 3056 AGGGCGCCGACGCTGGGAATTCGGGTTGCTGTGTCATTAACCGCCCACTAGT 2997  
Qy 5107 ATCGCATGTAAAGCCCACTGCAAGCTACTGCTTTCTTTTGCGCTTGCGTTTCCCTTG 5166  
Db 2996 ATCGCATGTAAAGCCCACTGCAAGCTACTGCTTTCTTTTGCGCTTGCGTTTCCCTTG 2937  
Qy 5167 TCCAGATAGCCCACTGCAAGCTACTGCAAGCTACTGCTTTCTTTTGCGCTTGCGTTTCCCTTG 5226  
Db 2936 TCCAGATAGCCCACTGCAAGCTACTGCAAGCTACTGCTTTCTTTTGCGCTTGCGTTTCCCTTG 2877  
Qy 5227 TCTACGTTTCCGCTTCTTTAGAGCGCTTGCGCCCTGAGTGTGTTGGGAGCGTG 5283  
Db 2876 TCTACGTTTCCGCTTCTTTAGAGCGCTTGCGCCCTGAGTGTGTTGGGAGCGTG 2820

RESULT 5  
US-10-811-028A-5  
; Sequence 5, Application US/10811028A  
; Publication No. US2005043258A1  
; GENERAL INFORMATION:  
; APPLICANT: Bennett, Michael  
; APPLICANT: Chen, Yen-Ju  
; APPLICANT: Genteric, Inc.  
; TITLE OF INVENTION: Methods of Treating Xerostomia and Xerophthalmia  
; FILE REFERENCE: 020714-002410US  
; CURRENT APPLICATION NUMBER: US/10/811,028A  
; PRIORITY FILING DATE: 2004-03-25  
; PRIOR APPLICATION NUMBER: US 60/458,793  
; PRIORITY FILING DATE: 2003-03-26  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: Patent Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 4058  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURES:  
; OTHER INFORMATION: Description of Artificial Sequence: pMB1-hTFN-alpha  
; OTHER INFORMATION: plasmid expression vector  
US-10-811-028A-5

Query Match 32.1%; Score 1697.8; DB 8; Length 4058;  
Best Local Similarity 86.7%; Pred. No. 0;  
Matches 1980; Conservative 0; Mismatches 102; Indels 201; Gaps 2;

Qy 2706 CTAGACGTAATCATGCTATAGCTGTTCCTGTGTGAATGTATTCGCTCAATTC 2765  
Db 1977 CTTGGCGTAATCATGCTATAGCTGTTCCTGTGTGAATGTATTCGCTCAATTC 2036  
Qy 2766 ACACAACTATGAGCGGGAACGATTAAGTGTAAAGCTGCGGTGCTTAATGAGTACTA 2825  
Db 2037 ACACAACTATGAGCGGGAACGATTAAGTGTAAAGCTGCGGTGCTTAATGAGTACTA 2096

Qy 2826 ACTCACTAATTAATGCTTGCGCTCACTGCGCGCTTTCAGTGCAGGAACCTGTGTCGA 2885  
Db 2097 ACTCACTAATTAATGCTTGCGCTCACTGCGCGCTTTCAGTGCAGGAACCTGTGTCGA 2156  
Qy 2886 GCTGCACTTAATGAAATGCGCAACGCGGGAAGAGCGGTTTGTGCTATTGGCGCTCTTC 2945  
Db 2157 GCTGCACTTAATGAAATGCGCAACGCGGGAAGAGCGGTTTGTGCTATTGGCGCTCTTC 2216  
Qy 2946 CGCTTCTCGCTCACTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3005  
Db 2217 CGCTTCTCGCTCACTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2276  
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Db 2397 CCATAGGCTCCGCCCCCTGACAGAGATCACAAAAATGACGCTCAAGTCAAGAGTGAGG 2456  
Qy 3186 AAACCCGACAGGACTAATAAGATACAGGCGTTTCCCTGGAAGCTCCCTGCGCTC 3245  
Db 2457 AAACCCGACAGGACTAATAAGATACAGGCGTTTCCCTGGAAGCTCCCTGCGCTC 2516  
Qy 3246 TCTGTTCCGACCCCTGCGCTTACCGGATACCTGTCGCTTTCCTTCCGGAAGCT 3305  
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Qy 3306 GCGGCTTCTCAATAGCTCAAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 3365  
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Qy 3366 GCTGCGCTGCTGACGAACCCCGCTTACGCGCGACCGCTGCGCTTATCCGTAATCA 3425  
Db 2637 GCTGCGCTGCTGACGAACCCCGCTTACGCGCGACCGCTGCGCTTATCCGTAATCA 2696  
Qy 3426 TCGTCTTGAATCCACCCGCTTAAGACAGACATTAATGCACTGAGCGAGCCACTGTGA 3485  
Db 2697 TCGTCTTGAATCCACCCGCTTAAGACAGACATTAATGCACTGAGCGAGCCACTGTGA 2756  
Qy 3486 CAGATTTAGCAGAGCGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 3545  
Db 2757 CAGATTTAGCAGAGCGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 2816  
Qy 3546 CTACGCTACACTAGAAAGACAGTATTTGATCTGCGCTGCTGCTGCTGCTGCTGCTGCT 3605  
Db 2817 CTACGCTACACTAGAAAGACAGTATTTGATCTGCGCTGCTGCTGCTGCTGCTGCTGCT 2876  
Qy 3606 CGGAAAAAGATTTGATGCTTTGATCCGCAAAACAACCGCTGCTGCTGCTGCTGCTGCT 3665  
Db 2877 CGGAAAAAGATTTGATGCTTTGATCCGCAAAACAACCGCTGCTGCTGCTGCTGCTGCT 2936  
Qy 3666 TTTTGTTCGACACAGCAAGTTAAGCGGCAAAAAAGATCTCAAGAGATCTTTGAT 3725  
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Qy 3726 CTTTTCACGGGCTGACGCTCAGTGAACGAAAACTACGTTAAGGATTTTGTGCTAT 3785  
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Qy 3846 GATGCGGATAGCCGCTGCTGCTTCTGATGCGGACGATTTGCACTGCCGTAGAA 3905  
Db 3060 ----- 3059  
Qy 3906 CTCGCGAGGTGCTCCAGCCTCAGGACGACCTGAACCACTTCGAGAGGAGTCAAGCCC 3965

Db 3060 -----CGATACATATTTGAATGATTTAGAAAATAACCAATAG 3100  
QY 3966 GGGGGGGCGAAGAACTCCAGATAGATCCCGGCTGGAGATCATCCAGCCGGCTC 4025  
Db 3101 GGGTTCCGGCACTTTCCCGAAAAGTCCACTGTATGGGTGTGAATAACCGCACAG 3160  
QY 4026 CCGGAAAACGATTCGGAAGCCCACTTTCATAGAAAGCGCGGTGAATCGAATCTCG 4085  
Db 3161 ATGGGTAGAGAAAATATCCCATCAGAAATTTGTAAGCTTAAAT----- 3208  
QY 4086 TGATGGCAGTTGGCGCTGCTTGTGTCATTTGAAACCCAGAGTCCGCTCAGAA 4145  
Db 3209 -----TCAGAA 3215  
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Db 3216 AACTGTCAAGAGCGCATAGAAAGCGATGCGCTGCGAATGGAGCGCGCATACCGTAA 3275  
QY 4206 AGCAGAGAAAGCGATCGCCCATTTGCGCGCAAGCTTTGAGCAATATCAAGGTAAGC 4265  
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Db 3456 TCCTCGCGGTCCGCGCATGCGCGCTTGAGCTGGCGAAGATTGGGCTGGCGAGCGCC 3515  
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Db 3516 TGATGCTTTTGTGTCAGATCATCTGATCGAAGACCGGCTTCATCCAGTACGTGCT 3575  
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QY 4626 AGGAGATCTGCGCCCGGCACTTTCGCAATAGCAGCGATCCCTTCCGCTTCAGTACA 4685  
Db 3696 AGGAGATCTGCGCCCGGCACTTTCGCAATAGCAGCGATCCCTTCCGCTTCAGTACA 3755  
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Db 3816 TCGTCTGCGAGTTCATTCAGGGGCGGGAAGGTCGCTTGAATAAAAGAACCGGCGCGC 3875  
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Db 3936 TCATAGCGGAATAGCTCTTCAACCGCAAGCGCGCGGAAGACTGCGGTGCAATCTTGT 3995  
QY 4926 TCATAGCGGAAGCATTCCTCATCTGTCTTGTGATCAGATCGATTCCTTCGCGCAT 4985  
Db 3996 TCATAGCGGAAGCATTCCTCATCTGTCTTGTGATCAGATTCCTTCGCGCAT 4055  
QY 4986 CAG 4988  
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Db 4056 CAG 4058  
RESULT 6  
US-10-811-028A-6  
; Sequence 6, Application US/10811028A  
; Publication No. US20050043258A1  
; GENERAL INFORMATION:  
; APPLICANT: Bennett, Michael  
; APPLICANT: Chen, Yen-Ju  
; APPLICANT: Genteric, Inc.  
; TITLE OF INVENTION: Methods of Treating Xerostomia and Xerophthalmia  
; FILE REFERENCE: 020714-002410US  
; CURRENT APPLICATION NUMBER: US/10/811,028A  
; PRIORITY FILING DATE: 2004-03-25  
; PRIOR FILING DATE: 2003-03-26  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 4187  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: pMB1-BesOD  
US-10-811-028A-6  
Query Match 32.1%; Score 1697.8; DB 8; Length 4187;  
Best Local Similarity 86.7%; Pred. No. 0;  
Matches 1980; Conservative 0; Mismatches 102; Indels 201; Gaps 2;  
QY 2706 CTAGAGCTATCATGCTGATAGCTGTTCTCTGTGTGAATTTGTTATCCGCTCACATTTCC 2765  
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QY 2766 ACACAAATACGAGCGCGGAAGCATTAAGTAAAGCCTGGGGGCTTAAGAGTAACTA 2825  
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QY 2946 CGCTTCCTGCTCACTGACCTGCGCTGCGCTGCTGCTGCTGCGGAGCGGTATGAC 3005  
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QY 3006 TCACCTCAAGCGCGTAAATACGTTATTCACAGATCAGGGATTAACGAGAAAGAAAT 3065  
Db 2406 TCACCTCAAGCGCGTAAATACGTTATTCACAGATCAGGGATTAACGAGAAAGAAAT 2465  
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Db 2526 CCAATAGGCTCGCGCCCTGACAGAGATCAAAAATTCAGCGCTCAAGTACAGAGTGGCG 2585  
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Db 2586 AAACCGGACAGACTAATAAGATACAGAGGCTTTCCCTGGAAGCTCCCTGCGCTC 2645  
QY 3246 TCTGTGTTCCGACCTGCGCTTACCGGATACCTGTCCGCTTTCTCTTCCGGAAGCGT 3305  
Db 2646 TCTGTGTTCCGACCTGCGCTTACCGGATACCTGTCCGCTTTCTCTTCCGGAAGCGT 2705  
QY 3306 GCGGCTTTCTCATAGCTCAGCGTGTAGGATCTCAATTCGCTGTAGTGTGCTGCCAA 3365  
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Db 2706 GGGGCTTTCTCAATGCTCAGCGCTGATAGTATCTCAGTTGAGTGGTGGTGGCTTCCAA 2765  
QY 3366 GCTGGGCTGTGTGACGCAACCCCCGCTTACGCGGACCGGTGGCCCTTATCCGGTAATA 3425  
Db 2766 GCTGGGCTGTGTGACGCAACCCCCGCTTACGCGGACCGGTGGCCCTTATCCGGTAATA 2825  
QY 3426 TCGCTTTGATGCAACCCCGGTAAAGACGACTTATCGCCACTGGACACCCACTGGTAA 3485  
Db 2826 TCGCTTTGATGCAACCCCGGTAAAGACGACTTATCGCCACTGGACACCCACTGGTAA 2885  
QY 3486 CAGGATTAGCAGACGAGATATGAGCGGTGCTACAGAGTCTTGAAGTGTGGCTTAA 3545  
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QY 4086 TGATGCAAGTTGGGCGCTCGCTTGTGTGTCATTTGCAACCCAGAGTCCCGCTCAGAG 4145  
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QY 4146 AACTCGTCAAGAAAGCGATGAAAGCGATGCGATCGGATCGGAGCGGATACCGTAA 4205  
Db 3345 AACTCGTCAAGAAAGCGATGAAAGCGATGCGATCGGATCGGAGCGGATACCGTAA 3404  
QY 4206 AGCAGAGAAAGCGGTGAGCCCATTCGCGCAAGCTTTCAAGCAATATCACGGTAAGCC 4265  
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QY 4266 AAGCGTATGCTGATAGCGGTCCGCCACACCCGCGGCGCACAGTGAATCCAGAA 4325  
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QY 4326 AAGCGGCAATTTTCCAGCATGATATTTGGCAAGAGGAGCATCGCATGGGTCAAGACAGA 4385  
Db 3525 AAGCGGCAATTTTCCAGCATGATATTTGGCAAGAGGAGCATCGCATGGGTCAAGACAGA 3584  
QY 4386 TCCTGCGGTGCGGCGATGCGGCGCTTGAAGCTGGCGAAGATTGAGTGGCGCGAGCCCC 4445

Db 3585 TCCTGCGGTGCGGCGATGCTGCGCTTGAGCTTGGCGAACAAGTTGCGGTGGCGGAGCCCC 3644  
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Db 3645 TGATGCTCTTTCGTCAGATCATCTGATGACAAAGCCGCTTCCATCCGAGTACGTGCT 3704  
QY 4506 CGCTGATGAGATGTTTCGCTTGGTGGTGAATGGGACAGGTAGCGGATCAAGCGTATGC 4565  
Db 3705 CGCTGATGAGATGTTTCGCTTGGTGGTGAATGGGACAGGTAGCGGATCAAGCGTATGC 3764  
QY 4566 AGCCGCGCATTTGCATCAGCCATGATGATPACTTTTCGCGCAGAGCAAGGTGATGAC 4625  
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QY 4686 AGGTGAGGACAGCTGCGAAGGAAAGCCCGTGGTGGCCAGCCAGATGACCGGCTGCC 4745  
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QY 4746 TCGTCTGCAAGTTCAATTCAGGGGCAACGAGTGGTCTTGA CAAAAAGAACCGGGCGC 4805  
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QY 4866 TCATAGCCGAATPAGCTCTCCACCAGGCGCGGAGAACTGCGTGAATCCATCTTGT 4925  
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QY 4926 TCATATATGGAAGATCTCATCTGCTCTTGAATCAGATCTTATCCCTGCGCAT 4985  
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QY 4986 CAG 4988  
Db 4185 CAG 4187

RESULT 7  
US-10-811-028A-2  
; Sequence 2, Application US/10811028A  
; Publication No. US20050043258A1  
; GENERAL INFORMATION:  
; APPLICANT: Bennett, Michael  
; APPLICANT: Chen, Yen-Jui  
; APPLICANT: Genetec, Inc.  
; TITLE OF INVENTION: Methods of Treating Xerostomia and Xerophthalmia  
; FILE REFERENCE: 020714-002410US  
; CURRENT APPLICATION NUMBER: US/10/811, 028A  
; PRIOR APPLICATION NUMBER: US 60/458, 793  
; PRIOR FILING DATE: 2003-03-26  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 4293  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: pMB1-HAMMSOD  
; OTHER INFORMATION: plasmid expression vector  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (1940)  
; OTHER INFORMATION: n = g, a, c or t  
US-10-811-028A-2

Query Match 32.1%; Score 1697.8; DB 8; Length 4293;





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QY 4866 TCATAGCGAATAGCTCTCCACCCAGCGCGGAGAACTGCGTCAATCCATTCTGT 4925
Db 4171 TCATAGCGAATAGCTCTCCACCCAGCGCGGAGAACTGCGTCAATCCATTCTGT 4230
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Db 4231 TCATATCTGGGAACGATCTCTATCTCTCTCTTGAATCAATCTTGAATCCCTGCGCAT 4290
QY 4986 CAG 4988
Db 4291 CAG 4293

RESULT 8
US-10-811-028A-1
; Sequence 1, Application US/10811028A
; Publication No. US20050043258A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Michael
; APPLICANT: Chen, Yen-Ju
; APPLICANT: Genetec, Inc.
; TITLE OR INVENTION: Methods of Treating Xerostomia and Xerophthalmia
; FILE REFERENCE: 020714-002410US
; CURRENT APPLICATION NUMBER: US/10/811,028A
; PRIOR FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US 60/458,793
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4332
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: pmB1-MmSOD
; OTHER INFORMATION: plasmid expression vector
; NAME/KEY: modified_base
; LOCATION: (1979)
; OTHER INFORMATION: n = g, a, c or t
US-10-811-028A-1

Query Match 32.1%; Score 1697.8; DB 8; Length 4332;
Best Local Similarity 86.7%; Pred. No. 0;
Matches 1980; Conservative 0; Mismatches 102; Indels 201; Gaps 2;

QY 2706 CTAGACGTATCATGTCATAGCTGTTTCTGTGTGAATTTTATCCGCTCACAATTCC 2765
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QY 2766 ACACAATCATGAGCGCGGAGGATTAAGTGAAGCCCTGGGGTGCCTTAATGAGAGCTA 2825
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Db 2371 ACTCACATTAATGCTGTTGCGCTCACTGCGCGCTTTCAGTCCGGAACCTGTGTCGA 2430
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QY 2946 CGCTTCTCGCTCACTGCTGCGCTGCGTGGTGGTGGTGGGAGAGCGGATACG 3005
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QY 3666 TTTTGTTCAGACAGACAGATTAACGCGGAGAAAAAGATCTCAAGAGATCCTTGAT 3725
Db 3211 TTTTGTTCAGACAGACAGATTAACGCGGAGAAAAAGATCTCAAGAGATCCTTGAT 3270
QY 3726 CTTTTCAGCGGCTCTGACGCTCAGTGAACGAAAATCAGCTTAAGGATTTGGTCA 3785
Db 3271 CTTTTCAGCGGCTCTGACGCTCAGTGAACGAAAATCAGCTTAAGGATTTGGTCA 3330
QY 3786 GAGATTATGTCGACCAAGCGGCAATGCTGCTCCCACTCCTGCAATTCGGGGCATG 3845
Db 3331 GAG----- 3333
QY 3846 GATGCGGATAGCGCTGCTGTTTCTGGAATGCCAGCATTTGCACTGCCGATAGA 3905
Db 3334 ----- 3333
QY 3906 CTCGCGAGGTGCTCAGCTCAGGACGAGTGAACCACTCGCGAGGGATCGAGCC 3965
Db 3334 ----- 3334
QY 3966 GGGGTGGCGAAGAACTCCAGCATGAGATCCCGCGCTGGAAGATATCAGCGCGGCTC 4025
Db 3375 GGGGTGGCGAAGAACTCCAGCATGAGATCCCGCGCTGGAAGATATCAGCGCGGCTC 3434
QY 4026 CCGGAAACGATTCGGAAGCCCACTTTCATAGAAAGCGGCGTGAATTCGAATCTCG 4085
Db 3435 ATGCGTAAGAGAAATACCGCATCAGAAATTTGTAAGCTTAATAT----- 3482
QY 4086 TGATGCGAGTTGGGCGTGGCTTGTGCTGATTTTGAACCCGAGATCCCGCTCAGA 4145
Db 3483 -----TCAAG 3489
QY 4146 AACTGCTCAAGAGCGGATGAGAGCGATGCGCTGCGAATCGGAGCGCGGATACGCTTA 4205
Db 3490 AACTGCTCAAGAGCGGATGAGAGCGGATGCGCTGCGAATCGGAGCGCGGATACGCTTA 3549
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QY 3606 CGAAAAAGATTGGTAGCTTTGATCCGAGCAACAAACACCGCTGTAGCGGTGTTT 3665
Db 4572 CGGAAAAAGATTGGTAGCTTTGATCCGAGCAACAAACACCGCTGTAGCGGTGTTT 4631
QY 3666 TTTTGTTCAGAGCAGCAGATTAACGCGAGAAAAAGATCTTCAGAAAGATCTTTGAT 3725
Db 4632 TTTTGTTCAGAGCAGCAGATTAACGCGAGAAAAAGATCTTCAGAAAGATCTTTGAT 4691
QY 3726 CTTTTCATACGGGGTCTGACGCTCAGTGAAGAAAACTCAGCTTAAGGATTTTGTGAT 3785
Db 4692 CTTTTCATACGGGGTCTGACGCTCAGTGAAGAAAACTCAGCTTAAGGATTTTGTGAT 4751
QY 3786 GAGATTAATCGTCAGCAAAAGCGCCATCGTGCCTCCCACTCCTGACGTTCCGGGGGATG 3845
Db 4752 GAG----- 4754
QY 3846 GATGCGGAGATGACCGCTGTGATTTCTGTGATGCGACGATTTTGACCTGCCGATGAA 3905
Db 4755 ----- 4754
QY 3906 CTCCCGAGAGTCTGTCAGACCTCAGAGCAGCTGAACCACTGCCAGGGGATCGAGCC 3965
Db 4755 -----CGATACATATTGTAATGTAATTGAAAAAATTAACAAATAG 4795
QY 3966 GGGGTGGGCGAAAGAACTCCAGCATGAGATCCCGCGCTGAGAGATCATCCAGCGCGTC 4025
Db 4796 GGGTTCGGCGCACTTTCCCGAAAAAGTCCACTGTATGGGTGTGAAATACCGCACAG 4855
QY 4026 CCGGAAAAAGATTCGGAAGCCCACTTTCAATAGAGCGCGGTGAATCGAAATCTCG 4085
Db 4856 ATGCGTAAGAGAAAAATACGCGCATACAGAAATGTAAACGTTAAT- 4903
QY 4086 TGATGGCAGGTGGGCGTCCGTTGTGTGATTTGCAACCCAGAGTCCCGCTCAGAG 4145
Db 4904 -----TCAGAG 4910
QY 4146 AACTCGTCAAGAAAGCGATAGAAAGCGATGCGCTGCGAATCGAGCGCGCATACCTAA 4205
Db 4911 AACTCGTCAAGAAAGCGATAGAAAGCGATGCGCTGCGAATCGAGCGCGCATACCTAA 4970
QY 4206 AGCAGAGAAAGCGGTGACCCCATTCGCGCCCAAGCTCTTCAGCAATATCACGGTAGCC 4265
Db 4971 AGCAGAGAAAGCGGTGACCCCATTCGCGCCCAAGCTCTTCAGCAATATCACGGTAGCC 5030
QY 4266 AAGCGTATGCTGATAGCGGTGCGGCACACCGAGCGCGCAGTGAATGAATCCAGAA 4325
Db 5031 AAGCGTATGCTGATAGCGGTGCGGCACACCGAGCGCGCAGTGAATGAATCCAGAA 5090
QY 4326 AAGCGGCATTTTCCACCATGATATTGCGCAAGCAGGATCGCATGGGTCAACGAGAG 4385
Db 5091 AAGCGGCATTTTCCACCATGATATTGCGCAAGCAGGATCGCATGGGTCAACGAGAG 5150
QY 4386 TCTTCGCGGTGCGGATGCGCGCTTGAAGCTTGCGCAACAGTTGGCTGGCGAGCC 4445
Db 5151 TCTTCGCGGTGCGGATGCGCGCTTGAAGCTTGCGCAACAGTTGGCTGGCGAGCC 5210
QY 4446 TGATGCTCTTGTGTCAGATCATCTGATCGACAAAGCGCTTCATCCGATGTCGTC 4505
Db 5211 TGATGCTCTTGTGTCAGATCATCTGATCGACAAAGCGCTTCATCCGATGTCGTC 5270
QY 4506 CGCTCGATGCGATTTTCGTTGGTGTGATGAGGAGGATGACCGATCAAGCGTATGC 4565
Db 5271 CGCTCGATGCGATTTTCGTTGGTGTGATGAGGAGGATGACCGATCAAGCGTATGC 5330
QY 4566 AGCGCGCGCATTCATGACGATGATGATCTTTCTGCGAGAGCAAGGTGATGATGAC 4625
Db 5331 AGCGCGCGCATTCATGACGATGATGATCTTTCTGCGAGAGCAAGGTGATGATGAC 5390
QY 4626 AGGAGATTCGCGCGCGCATTCGCGCAATAGCAGCGAGTCCCTCCGCTTCAGTACA 4685
Db 5391 AGGAGATTCGCGCGCGCATTCGCGCAATAGCAGCGAGTCCCTCCGCTTCAGTACA 5450
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QY 4686 AGCTGAGCAGCAGCTGCGAGAGAAAGCCCGTCTGTGGCAGCCACGATAGCCGCTGCC 4745
Db 5451 AGCTGAGCAGCAGCTGCGAGAGAAAGCCCGTCTGTGGCAGCCACGATAGCCGCTGCC 5510
QY 4746 TCGTCTGCAATTCATTCAGGGGACCGGACAGGTGCGTCTTGAACAAAGAAACCGGGCG 4805
Db 5511 TCGTCTGCAATTCATTCAGGGGACCGGACAGGTGCGTCTTGAACAAAGAAACCGGGCG 5570
QY 4806 CCGTGGCGTGAAGCCCGGAAACCGGGGATCAGACACCGATTCGATTGTGGCCAG 4865
Db 5571 CCGTGGCGTGAAGCCCGGAAACCGGGGATCAGACACCGATTCGATTGTGGCCAG 5630
QY 4866 TCATAGCCGAATAGCTCTCCACCCAGAGCGCGCGAGAACTGCGTGAATCCATCTGT 4925
Db 5631 TCATAGCCGAATAGCTCTCCACCCAGAGCGCGCGAGAACTGCGTGAATCCATCTGT 5690
QY 4926 TCATATGCGAAAGCATCTCATCTGTCTTTGATCAGATTTGATCCCTGCGCCAT 4985
Db 5691 TCATATGCGAAAGCATCTCATCTGTCTTTGATCAGATTTGATCCCTGCGCCAT 5750
QY 4986 CAG 4988
Db 5751 CAG 5753

RESULT 10
US-10-811-028A-4
; Sequence 4, Application US/10811028A
; Publication No. US20050043258A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Michael
; APPLICANT: Chen, Yen-Ju
; APPLICANT: Generic, Inc.
; TITLE OF INVENTION: Methods of Treating Xerostomia and Xerophthalmia
; FILE REFERENCE: 020714-002410US
; CURRENT APPLICATION NUMBER: US/10/811,028A
; PRIOR FILING DATE: 2004-03-25
; PRIOR FILING DATE: 2003-03-26
; NUMBER OF SEQ. ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 5760
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: pMB1-Mt-CAT
; OTHER INFORMATION: Plasmid expression vector
; US-10-811-028A-4

Query Match 32.1%; Score 1697.8; DB 8; Length 5760;
Best local Similarity 86.7%; Pred. No. 0;
Matches 1980; Conservative 0; Mismatches 102; Indels 201; Gaps 2;

QY 2706 CTAGAGTAATCATGTCATAGCTGTTCTCTGTGAAATTTGTTATCCGTCACAAATTC 2765
Db 3679 CTAGAGTAATCATGTCATAGCTGTTCTCTGTGAAATTTGTTATCCGTCACAAATTC 3738
QY 2766 ACAACAATACGAGCGCGGAAAGCAATAAGTAAAGCTGGGGGCTTAATGATGAGCTTA 2825
Db 3739 ACAACAATACGAGCGCGGAAAGCAATAAGTAAAGCTGGGGGCTTAATGATGAGCTTA 3798
QY 2826 ACTCACATTAATTTGCTTGGCTCACTGCGCTTTCAGTCCGGAACCTGTGCGCA 2885
Db 3799 ACTCACATTAATTTGCTTGGCTCACTGCGCTTTCAGTCCGGAACCTGTGCGCA 3858
QY 2886 GCTGCAATTAATGATGCGCCACGCGCGGAGAGGCGGTTTTCGTAATTTGGCGCTCTTC 2945
Db 3859 GCTGCAATTAATGATGCGCCACGCGCGGAGAGGCGGTTTTCGTAATTTGGCGCTCTTC 3918
QY 2946 CGCTTCCTGCTCACTGACCTGCTGCGTCCGTCGTTCCGCTGCGCGAGCGGTATCAG 3005
Db 3919 CGCTTCCTGCTCACTGACCTGCTGCGTCCGTCGTTCCGCTGCGCGAGCGGTATCAG 3978
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; TITLE OF INVENTION: VECTOR
; FILE REFERENCE: 00801017900US00
; CURRENT APPLICATION NUMBER: US/10/286,186
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US/09/505,477
; PRIOR FILING DATE: 2000-02-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 5225
; TYPE: DNA
; ORGANISM: Porcine Circovirus
US-10-286-186-16

Query Match      32.0%; Score 1692.4; DB 6; Length 5225;
Best Local Similarity 82.7%; Pred. No. 0;
Matches 208; Conservative 0; Mismatches 206; Indels 231; Gaps 4;

QY      2942 CTTCCGCTTCTCGCTCACTGACTCGCTGCGCTCGTTCGTTCCGCTCGCGGAGCGGTAT 3001
Db      5225 CTTCCGCTTCTCGCTCACTGACTCGCTGCGCTCGTTCGTTCCGCTCGCGGAGCGGTAT 5166

QY      3002 CAGTCACTCAAGGCGGTATACGGTTATTCACAGATCAAGGAGTAAACGAGAAAGA 3061
Db      5165 CAGTCACTCAAGGCGGTATACGGTTATTCACAGATCAAGGAGTAAACGAGAAAGA 5106

QY      3062 ACATGTAGCAAAAGGCGAGCAAAAGGCGAGAAACGGTAAAGGCGCGTTCGTCGCT 3121
Db      5105 ACATGTAGCAAAAGGCGAGCAAAAGGCGAGAAACGGTAAAGGCGCGTTCGTCGCT 5046

QY      3122 TTTTCCATAGAGCTCGGCCCCCTGACAGCATCAAAAAATCGACGCTCAAGTCAGAGT 3181
Db      5045 TTTTCCATAGAGCTCGGCCCCCTGACAGCATCAAAAAATCGACGCTCAAGTCAGAGT 4986

QY      3182 GGGCAAAACCCGACAGGACTATAAGATACCAAGGCGTTCCCGCTGAGAACTCCCTCGTGC 3241
Db      4985 GGGCAAAACCCGACAGGACTATAAGATACCAAGGCGTTCCCGCTGAGAACTCCCTCGTGC 4926

QY      3242 GCTCTCTGTTCCGACCGCTGCGCTTACCGGATPACTGTCGCGCTTCTCCCTTCGAGAA 3301
Db      4925 GCTCTCTGTTCCGACCGCTGCGCTTACCGGATPACTGTCGCGCTTCTCCCTTCGAGAA 4866

QY      3302 GCGTGGCGCTTCTCATAGCTCAGCTGTAGATCTCAAGTTCGGTGTAGGTCGTTGCT 3361
Db      4865 GCGTGGCGCTTCTCATAGCTCAGCTGTAGATCTCAAGTTCGGTGTAGGTCGTTGCT 4806

QY      3362 CCAAGCTGGGCTGTGTGACGAAACCCCGCTTACGCGCCGACCGTGGCGCTTATCCGCTA 3421
Db      4805 CCAAGCTGGGCTGTGTGACGAAACCCCGCTTACGCGCCGACCGTGGCGCTTATCCGCTA 4746

QY      3422 ACTATCGTCTTGAAGTCCGAGCCGCTTAAAGACAGCACTTATCGCCACTGGACAGCACTG 3481
Db      4745 ACTATCGTCTTGAAGTCCGAGCCGCTTAAAGACAGCACTTATCGCCACTGGACAGCACTG 4686

QY      3482 GTAAACAGATTTAGAGAGCAAGATATGTAGGCGGTGTACTACAGATTTCTTGAAGTGTGC 3541
Db      4685 GTAAACAGATTTAGAGAGCAAGATATGTAGGCGGTGTACTACAGATTTCTTGAAGTGTGC 4626

QY      3542 CTAACTACGGCTACACTTAAGAAAGCACTATTTGGTATCTGCGCTCTCTCTGAAGCACTTA 3601
Db      4625 CTAACTACGGCTACACTTAAGAAAGCACTATTTGGTATCTGCGCTCTCTCTGAAGCACTTA 4566

QY      3602 CTTTCGAGAAAAGATTGTAGTCTTGTATCCGCAAAACCAACCGCTGTGTAGCGGTG 3661
Db      4565 CTTTCGAGAAAAGATTGTAGTCTTGTATCCGCAAAACCAACCGCTGTGTAGCGGTG 4506

QY      3662 GTTTTTTTTGTGACAGCAGATTAACGGCAGAAAAAAGATCTCAAGAAATCTT 3721
Db      4505 GTTTTTTTTGTGACAGCAGATTAACGGCAGAAAAAAGATCTCAAGAAATCTT 4446

QY      3722 TGATCTTTTCTAAGGGGTGTAGCGCTCAGTGAAGCAAGAACTCAGCTTAAGGATTTTGG 3781
Db      4445 TGATCTTTTCTAAGGGGTGTAGCGCTCAGTGAAGCAAGAACTCAGCTTAAGGATTTTGG 4386
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QY      3782 TCATGAGATTATC----- 3794
Db      4385 TCATGAGATTATCAAAAAGATCTTCACCTAATCTTTAAATTAAATGAAGTTTA 4326

QY      3795 -----GTGACCA 3802
Db      4325 GCACGTGTACGTCTCTCTCGGCCACGAGTGTACCGAGTTCCGCGCGGAGTCCGCA 4266

QY      3803 AAGCGGCATCTGTGCTTCCCACTCTGTGAGTTCCGGGGCAATGATCCCGATGCGCC 3862
Db      4265 GAGCGCAATCTCCGCCCCACGCGTGTCCGATCTGGTCAATGCGCGGCGCGAGCT 4206

QY      3863 TGCTGTTTCTGATATCGAGATTTGCACTGCGGAGTAACTCCGAGATGCTGTCA 3922
Db      4205 CCGGAAATTCGTGTGACACGACTCCGACCATTCGCGGTACAGCTGTGTCAAGCGCGCA 4146

QY      3923 GCC----- 3925
Db      4145 CCACACCCAGGACAGGTTGTCCGACCACTGTCTGTGACCGCGCTGATGAACA 4086

QY      3926 ---TCAGCAGCAGCTGAACCACTCGAGAGGAGTCCAGCCGGGGTGGGGAAGACT 3982
Db      4085 GGGTCACTGTCTCGGACCAACCGGGAAGTCTCTCCACGAAATCCGGAGAACCC 4026

QY      3983 CCAGCATG-----AGATCCCCGCGTGGAGATCATCCAGCCGCGCTC 4025
Db      4025 CGAGCTGTGCAACTTGGCATGTGTGCGCTCTCTCACTGTATTAATTAACATTTATC 3966

QY      4026 CCGAAAAAGATTCGAGACCCCACTTTCATTAAGAAAGCGCGGTGGAATCGAAATCTG 4085
Db      3965 AGGTATATTGTCTCATAGACCGATACATTTGAATGTATTAAGAAATTAACAATAG 3906

QY      4086 TGATGCAAGTTGGGGGTGCTGTGTGCTGTCAATTTCGAACCCCAAGTCCCGC----- 4138
Db      3905 GGGTTCGCGCACTTTCCCGAAAAGTGCACCTGTATCGGTGTGAATTCGCGACG 3846

QY      4139 -----TCAGAAAGACTC 4150
Db      3845 ATGCGTAAGAGAAAATACCGCATCAGAAATTTGAAGCTTAATTAATTCAGAAAGACTC 3786

QY      4151 GTCAAGAAAGCGATTAAGAAAGCGATGTGCGTCCGAATGTGGAGCGCGGATTCGGTAAAGCAC 4210
Db      3785 GTCAAGAAAGCGATTAAGAAAGCGATGTGCGTCCGAATGTGGAGCGCGGATTCGGTAAAGCAC 3726

QY      4211 GAGGAAGGAGTGAAGCCATTGCGCGGCAAGCTCTTCAGCAATATCAAGGATGCCAAGC 4270
Db      3725 GAGGAAGGAGTGAAGCCATTGCGCGGCAAGCTCTTCAGCAATATCAAGGATGCCAAGC 3666

QY      4271 TATGTCCTGATAGCGGTCCGCCACACCCAGCGGCGACAGTGTGATTCAGAAAAGCG 4330
Db      3665 TATGTCCTGATAGCGGTCCGCCACACCCAGCGGCGACAGTGTGATTCAGAAAAGCG 3606

QY      4331 GCCATTTTCCACATATATTTGGGCAAGCAGCATGTGGCTACAGAGATCTCTC 4390
Db      3605 GCCATTTTCCACATATATTTGGGCAAGCAGCATGTGGCTACAGAGATCTCTC 3546

QY      4391 GCGGTGGGCAATGCGGCGCTTGAAGCTGTGCGAAAGTTGCGGTGGGCGAGGCCCTGATG 4450
Db      3545 GCGGTGGGCAATGCTGCTTGAAGCTGTGCGAAAGTTGCGGTGGGCGAGGCCCTGATG 3486

QY      4451 CTCCTTCGTCAGATCATCTGTATCGACAAAGCCGCTTCAATCCAGTACGTCTGCTC 4510
Db      3485 CTCCTTCGTCAGATCATCTGTATCGACAAAGCCGCTTCAATCCAGTACGTCTGCTC 3426

QY      4511 GATGCAATTTTTCGCTTGTGTGCTGAATGGGCAAGTATGCGGATCAAGGCTATGACCGG 4570
Db      3425 GATGCAATTTTTCGCTTGTGTGCTGAATGGGCAAGTATGCGGATCAAGGCTATGACCGG 3366

QY      4571 CCGCATTTGATGACCATGATGATCTTTCTTCGCGAGGACGAAGGTGAGATGACGAGAG 4630
Db      3365 CCGCATTTGATGACCATGATGATCTTTCTTCGCGAGGACGAAGGTGAGATGACGAGAG 3306
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QY 4631 ATCTGCCCCGCACTTCCGCCAATAGACGCAATGCTTCCCGCTTCAATGACAACTG 4690  
Db 3305 ATCTGCCCCGCACTTCCGCCAATAGACGCAATGCTTCCCGCTTCAATGACAACTG 3246  
QY 4691 GAGCAGAGTGGCGAAGGAAGCCCGTGGCGCGCAAGATCCCGGCTGCTGCTGCTG 4750  
Db 3245 GAGCAGAGTGGCGAAGGAAGCCCGTGGCGCGCAAGATCCCGGCTGCTGCTGCTG 3186  
QY 4751 CTGCACTTCAATCAGGCGACCGGACAGTGGCTTCTTGAACAAAAGAACCGGCGCGCTG 4810  
Db 3185 TTGCACTTCAATCAGGCGACCGGACAGTGGCTTCTTGAACAAAAGAACCGGCGCGCTG 3126  
QY 4811 CGCTGACAGCGGAAACAGCGCGGCAATCAGAGAGCGGATTTGCTTTGCTGCGCACTA 4870  
Db 3125 CGCTGACAGCGGAAACAGCGCGGCAATCAGAGAGCGGATTTGCTTTGCTGCGCACTA 3066  
QY 4871 GCCGAATGCTCTCCACCCAGCGGCGGAGAACCTGCTGCAATCCATCTTTGCTCAAT 4930  
Db 3065 GCCGAATGCTCTCCACCCAGCGGCGGAGAACCTGCTGCAATCCATCTTTGCTCAAT 3006  
QY 4931 CATGCGAAGCGATCTCACTCTGCTCTTGTATCAGATCTTGAATCCGCGCATCAGAT 4990  
Db 3005 CATGCGAAGCGATCTCACTCTGCTCTTGTATCAGATCTTGAATCCGCGCATCAGAT 2946  
QY 4991 CTTGCGCGGCAAGAAAGCCATCAGTTACTTTGAGGAGCTTCCCACTTACAGAGG 5050  
Db 2945 CTTGCGCGGCAAGAAAGCCATCAGTTACTTTGAGGAGCTTCCCACTTACAGAGG 2886  
QY 5051 CGCCCACTGCGCAATTCGCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5110  
Db 2885 CGCCCACTGCGCAATTCGCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2826  
QY 5111 CCATGTAAGCCCACTGCAAGCTACTGCTTCTCTTGGCGCTTGGCTTCCCTGCTGCA 5170  
Db 2825 CCATGTAAGCCCACTGCAAGCTACTGCTTCTCTTGGCGCTTGGCTTCCCTGCTGCA 2766  
QY 5171 GATAGCCCACTGATGATGATTCATTCGCGGATCAGACCGTTTCTGCGGACTGCTTCTA 5230  
Db 2765 GATAGCCCACTGATGATGATTCATTCGCGGATCAGACCGTTTCTGCGGACTGCTTCTA 2706  
QY 5231 CGTG 5234  
Db 2705 CGTG 2702

RESULT 12  
US-10-790-455-10/c  
; Sequence 10, Application US/10790455  
; Publication No. US20040210954A1  
; GENERAL INFORMATION:  
; APPLICANT: Avigenics, Inc  
; TITLE OF INVENTION: Avian Integrase-mediated Transformation  
; FILE REFERENCE: A181 1080.1  
; CURRENT APPLICATION NUMBER: US/10/790, 455  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 10  
; LENGTH: 6233  
; TYPE: DNA  
; ORGANISM: Plasmid PCR-XL-TOPO-CMV-pur-actb  
US-10-790-455-10

Query Match 30.9%; Score 1634.4; DB 8; Length 6233;  
Best Local Similarity 80.6%; Pred. No. 0;  
Matches 2082; Conservative 0; Mismatches 211; Indels 291; Gaps 3;

QY 2942 CTTCCGCTTCTCTGCTCACTGACTCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3001  
Db 6233 CTTCCGCTTCTCTGCTCACTGACTCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6174  
QY 3002 CAGCTCACTCAAGCGGTAAATACGTTATCAGAGATCAGGAGATTAACGAGAAAGA 3061

Db 6173 CAGCTCACTCAAGCGGTAAATACGTTATCAGAGATCAGGAGATTAACGAGAAAGA 6114  
QY 3062 ACATGTGACAAAAGGCGGAGAAAAGCCAGAAAACCGTAAAGGCGCGCTTGCCTGCGCT 3121  
Db 6113 ACATGTGACAAAAGGCGGAGAAAAGCCAGAAAACCGTAAAGGCGCGCTTGCCTGCGCT 6054  
QY 3122 TTTTCCATAGGCTCGCGCCCGCTGACAGCATCAAAAATTCAGCTCAAGTCAGAGGT 3181  
Db 6053 TTTTCCATAGGCTCGCGCCCGCTGACAGCATCAAAAATTCAGCTCAAGTCAGAGGT 5994  
QY 3182 GCGCAACCCGACAGAGATTAAGATACAGGCGTTTCCCTCTGAAAGCTTCCCTGCTG 3241  
Db 5993 GCGCAACCCGACAGAGATTAAGATACAGGCGTTTCCCTCTGAAAGCTTCCCTGCTG 5934  
QY 3242 GCTCTCCGTTCCGACCCCTGCGGCTTACCGGATACCTGCTCCGCTTTCCTTCCGGA 3301  
Db 5933 GCTCTCCGTTCCGACCCCTGCGGCTTACCGGATACCTGCTCCGCTTTCCTTCCGGA 5874  
QY 3302 GCGTGGCGCTTCTCATAGCTCAAGCTGTAGATCTCAGTTCCGATGAGTCCGCT 3361  
Db 5873 GCGTGGCGCTTCTCATAGCTCAAGCTGTAGATCTCAGTTCCGATGAGTCCGCT 5814  
QY 3362 CCAAGCTGGGCTGTGTGACGAAACCCCGCTTACGCGCGACCGCTGCTTATCCGTA 3421  
Db 5813 CCAAGCTGGGCTGTGTGACGAAACCCCGCTTACGCGCGACCGCTGCTTATCCGTA 5754  
QY 3422 ACTATCGTCTTGAATCCAAACCGGTAAGACACGATTAATGCGCACTGGACAGCACTG 3481  
Db 5753 ACTATCGTCTTGAATCCAAACCGGTAAGACACGATTAATGCGCACTGGACAGCACTG 5694  
QY 3482 GTAACAGATTAAGAGAGAGAGATATGATGAGCGGTGCTACAGATTTCTTGAAGTGTGG 3541  
Db 5693 GTAACAGATTAAGAGAGAGAGATATGATGAGCGGTGCTACAGATTTCTTGAAGTGTGG 5634  
QY 3542 GTAACTACGCTACACTAGAAAGAACAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3601  
Db 5633 GTAACTACGCTACACTAGAAAGAACAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5574  
QY 3602 CTTTCCGAAAAGATTTGATGCTTGTATTCGCGCAACCAACCGCTGTGTGCGGTG 3661  
Db 5573 CTTTCCGAAAAGATTTGATGCTTGTATTCGCGCAACCAACCGCTGTGTGCGGTG 5514  
QY 3662 GTTTTTTGTGTAAGCAGAGATTAAGCGGCGAAGAAAAGATCTCAAGAAATCCTT 3721  
Db 5513 GTTTTTTGTGTAAGCAGAGATTAAGCGGCGAAGAAAAGATCTCAAGAAATCCTT 5454  
QY 3722 TGATCTTTTCTACCGGCTCTGACGCTCAGTGAAGCAAACTCAGCTTAAAGGATTTGG 3781  
Db 5453 TGATCTTTTCTACCGGCTCTGACGCTCAGTGAAGCAAACTCAGCTTAAAGGATTTGG 5394  
QY 3782 TCATGAGATTATC----- 3794  
Db 5393 TCATGAGATTATCAAAAAGATCTTCACTAGATCTTTTAAATTAATAAGATTTTA 5334  
QY 3795 -----GTGACCA 3802  
Db 5333 GCAAGTGTACGCTCTGCTCTCTCGGCAAGATGACGCAAGTGGCGGCGGCGGCGGCA 5274  
QY 3803 AAGCGGCATCTGCTGCT 3862  
Db 5273 GGGGGAACCTCGCGCCCGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 5214  
QY 3863 TGCTGCTTCTCTGATGCGGAGATTTGCACTGCGGCTGAACTCCGCGAGTCTGCA 3922  
Db 5213 CCGGGAAGTTCGTGACACGACCTCGGCAACACTCGGCTGACAGCTGTCAGGCGCGGCA 5154  
QY 3923 GCC----- 3925  
Db 5153 CCAACACCAAGCGAGGCTTTCTCGGCAACACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5094  
QY 3926 ---TCAAGCAGAGCTGAACCACTGCGAGGAGATCGAGCCCGGCTGCGGCAAGACT 3982  
Db 5093 GGGTCACTGCTCGCGGACCAACCGGCAAGTCTCTCAAGAGTCCCGGAGAAC 5034





QY 3302 GCGTGGCGCTTTCTCATAGCTCAAGCTGATGATCTCAGTTGCGTAGTGCTGCT 3361  
 DB 5873 GGGTGGCGCTTTCTCATAGCTCAAGCTGATGATCTCAGTTGCGTAGTGCTGCT 5814  
 QY 3362 CCAAGCTGGGCTGTGTGCAAGAAACCCCGTTACGCCCAAGCTGCGCTTATCCGGTA 3421  
 DB 5813 CCAAGCTGGGCTGTGTGCAAGAAACCCCGTTACGCCCAAGCTGCGCTTATCCGGTA 5754  
 QY 3422 ACTATGCTTGTAGTCCAAACCGGTTAAGACAGACTTATCGCACTGGAGAGCAAGCTG 3481  
 DB 5753 ACTATGCTTGTAGTCCAAACCGGTTAAGACAGACTTATCGCACTGGAGAGCAAGCTG 5694  
 QY 3482 GTAACAGATTAGCAGAGGAGATATGATGAGCGTGTCTACAGATTCTTGAAGTGTGC 3541  
 DB 5693 GTAACAGATTAGCAGAGGAGATATGATGAGCGTGTCTACAGATTCTTGAAGTGTGC 5634  
 QY 3542 CTAACTACCGGCTACACTAGAAAGACATATTTGATCTGCGCTGTCTGAAGCCAGTTA 3601  
 DB 5633 CTAACTACCGGCTACACTAGAAAGACATATTTGATCTGCGCTGTCTGAAGCCAGTTA 5574  
 QY 3602 CTTGCGAAAAAGATTGGTAGCTCTGATCCGGCAACAAACACCGCTGTGTAAGCTG 3661  
 DB 5573 CTTGCGAAAAAGATTGGTAGCTCTGATCCGGCAACAAACACCGCTGTGTAAGCTG 5514  
 QY 3662 GTTTTTTTTGTGCAAGCAGATTACCGCAAGAAAAAGATCTCAAGAAATCTT 3721  
 DB 5513 GTTTTTTTTGTGCAAGCAGATTACCGCAAGAAAAAGATCTCAAGAAATCTT 5454  
 QY 3722 TGATCTTTTCTACGGGGTCTGACGCTCAGTGAACGAAAACTCACGTTAAGGATTTGG 3781  
 DB 5453 TGATCTTTTCTACGGGGTCTGACGCTCAGTGAACGAAAACTCACGTTAAGGATTTGG 5394  
 QY 3782 TCATGAGATTATC----- 3794  
 DB 5393 TCATGAGATTATCAAAAAAGATCTTCACTAGATCTTTTAAATTAAGAGTTTA 5334  
 QY 3795 -----GTGACCA 3802  
 DB 5333 GCAAGTGCAGTCTGCTCTCTCGGCACAGAAATGACACGATGCGCGCGCGGTGCGCA 5274  
 QY 3803 AAGCGGCATGTCGCTCTCCCACTCTGCAAGTTGCGGGGCGATGATGCGCGGATAGCGC 3862  
 DB 5273 GGGCGAATCTCCGCGCCCGACGCGCTGCTCGCGATCTCGGTCAATGCGCGCGCGGCGT 5214  
 QY 3863 TGCTGTTTCTCGAATGCGGACGATTTTGCACTGCGCGTGAAGAACTCCCGAGGTGTCA 3922  
 DB 5213 CCGGAAATGCTGAGACACGACCTCCGACCACTCGGCTGACAGCTCTGTCAGGCGCGCA 5154  
 QY 3923 GGC----- 3925  
 DB 5153 CCGACACCCAGGCGAGGTGTTGTCGGGACCACTGCTGATGATGATGAAACA 5094  
 QY 3926 ---TCAGGACAGAGTGAACCAACTCGCGAGGGATGAGCCCGGGGTGGCGAAGAACT 3982  
 DB 5093 GGGTCACTGCTCTCCGAGCACACCGCGGAAGTCTCTTCCAGGAATGCCGGGAGAAC 5034  
 QY 3983 CCAAGATGAGATCCCGCGCTGAGAGATCATTCAGCCGCGCTCCGGAAGAGATTCGCA 4042  
 DB 5033 CGAGCCGCTGCTGACAGAACTGACCGCTCCGGGACAGCTGCGCGCGGTGAGCAACCGAA 4974  
 QY 4043 AGCCCAACTTTTCAATAGAAAGCGCGGTGAATCGAAATCTCGTATGAGGAGTTGGCG 4102  
 DB 4973 CGGCACTGCTCACTGGGCACTGATGAGCCCTCTCAAGCTGCTATTTATGAAGCAATTA 4914  
 QY 4103 TCGCTTGTGCTCAATTTGAAACCCAGAGTCCG----- 4137  
 DB 4913 AGGGTATTTGTCTATGAGCGGATACATATTTGAATGATTTAGAAAAATTAACAAATAG 4854  
 QY 4138 ----- 4137  
 DB 4853 GGGTTCGCGCAATTTCCCGAAAAATGCGCACTGTATGCGGTGTAATACCGCAAG 4794  
 QY 4138 -----CTCAGAAAGATC 4150

DB 4793 ATGCGTAAGGAAAAATACCGCATCAGAAATTTGTAAGCTTAAATTCAGAAATCTC 4734  
 QY 4151 GTCAAGAAAGCGATAGAAAGCGATGCTGCGAATCGGAGCGGATACCGTAAGAC 4210  
 DB 4733 GTCAAGAAAGCGATAGAAAGCGATGCTGCGAATCGGAGCGGATACCGTAAGAC 4674  
 QY 4211 GAGAAAGGCTCAGGCCATTTGGCCCGCAAGCTCTTCAAGATATACGGGTAGCCAGC 4270  
 DB 4673 GAGAAAGGCTCAGGCCATTTGGCCCGCAAGCTCTTCAAGATATACGGGTAGCCAGC 4614  
 QY 4271 TATGCTGATGAGCGGTCCGCAACACCGCGCGGCAAGTGGATGATCCAGAAAGG 4330  
 DB 4613 TATGCTGATGAGCGGTCCGCAACACCGCGCGGCAAGTGGATGATCCAGAAAGG 4554  
 QY 4331 GCCATTTTCAACATGATATTTGCGAAGCAGGATCGCATAGGTCAAGAGAGATCTTC 4390  
 DB 4553 GCCATTTTCAACATGATATTTGCGAAGCAGGATCGCATAGGTCAAGAGATCTTC 4494  
 QY 4391 GCCGTGGGCAATGCGCGCTTGAAGCTGCGCAAGATTGCGCTGCGCGAGCCCTGATG 4450  
 DB 4493 GCCGTGGGCAATGCGCGCTTGAAGCTGCGCAAGATTGCGCTGCGCGAGCCCTGATG 4434  
 QY 4451 CTCTTCGTCAGATCATCTGATGCAAGACCGGCTTCAATCGAGTAAGTGTGCTGCTC 4510  
 DB 4433 CTCTTCGTCAGATCATCTGATGCAAGACCGGCTTCAATCGAGTAAGTGTGCTGCTC 4374  
 QY 4511 GATGCGATGTTTCTGTTGATGATGAGGAGGAGTACCGGATCAAGCGTATGAGCGC 4570  
 DB 4373 GATGCGATGTTTCTGTTGATGATGAGGAGGAGTACCGGATCAAGCGTATGAGCGC 4314  
 QY 4571 CCGCATTTGATCAGCATGATGATGATCTTTCTGCGAGAGCAAGTGAATGACAGAG 4630  
 DB 4313 CCGCATTTGATCAGCATGATGATGATCTTTCTGCGAGAGCAAGTGAATGACAGAG 4254  
 QY 4631 ATCCGCGCGGCACTTCGCGCAATGAGAGCGAGTCCCTGCGCTTCAAGAACAGTGC 4690  
 DB 4253 ATCCGCGCGGCACTTCGCGCAATGAGAGCGAGTCCCTGCGCTTCAAGAACAGTGC 4194  
 QY 4691 GAGCAAGCTGCGCAAGAAACGCGCTGTTGAGGACGACAGATAGCGCGCTGCTGCTC 4750  
 DB 4193 GAGCAAGCTGCGCAAGAAACGCGCTGTTGAGGACGACAGATAGCGCGCTGCTGCTC 4134  
 QY 4751 CTGAGATTCAATTCAGGCACTGACAGGTGCTTGAAGAAAGAACCGGCGCCCTG 4810  
 DB 4133 TTGAGATTCAATTCAGGCACTGACAGGTGCTTGAAGAAAGAACCGGCGCCCTG 4074  
 QY 4811 CGCTGACGCGGAAACAGCGGCGCATCAGAGCAGCGGATGCTGTTGTCGCGATCA 4870  
 DB 4073 CGCTGACGCGGAAACAGCGGCGCATCAGAGCAGCGGATGCTGTTGTCGCGATCA 4014  
 QY 4871 GCCGAATAGCTCTCAACCAAGCGCGGAGAACCTGCGTCAATCAATCTTTCAT 4930  
 DB 4013 GCCGAATAGCTCTCAACCAAGCGCGGAGAACCTGCGTCAATCAATCTTTCAT 3954  
 QY 4931 CATGCGAAAGATCTTATCTGCTCTTGAATGATCTTGAATCCCTGCGCATCAAT 4990  
 DB 3953 CATGCGAAAGATCTTATCTGCTCTTGAATGATCTTGAATCCCTGCGCATCAAT 3894  
 QY 4991 CTTGCGGCGGAAAGACCATCAAGTTTACTTTGACAGGCGCTCCCACTTACAGAGGG 5050  
 DB 3893 CTTGCGGCGGAAAGACCATCAAGTTTACTTTGACAGGCGCTCCCACTTACAGAGGG 3834  
 QY 5051 CGCCCAAGCTGCAATTCGAGTTGCTGCTGCTGATCAATAAACCGCAAGTCAAGTATG 5110  
 DB 3833 CGCCCAAGCTGCAATTCGAGTTGCTGCTGCTGATCAATAAACCGCAAGTCAAGTATG 3774  
 QY 5111 CCAATGTAAGCCCACTGCAAGCTGCTTCTTCTTGGCGCTTGGCTTCTCTGCTCA 5170  
 DB 3773 CCAATGTAAGCCCACTGCAAGCTGCTTCTTCTTGGCGCTTGGCTTCTCTGCTCA 3714  
 QY 5171 GATAGCCCAATGATGATCAATCCGAGGTGAGACCGGTTCTGCGGAGATGAGCTTCTA 5230

Db 3713 GATAGCCAGTAGCTGACATTCATCCGGGTGACGACCGTTTCTGCGGACTGCTTTCTA 3654  
Qy 5231 CGTG 5234  
Db 3653 CGTG 3650

RESULT 14  
US-10-940-315-10/c  
: Sequence 10, Application US/10940315  
: Publication No. US20050034186A1  
: GENERAL INFORMATION:  
: APPLICANT: Avigenics, Inc  
: TITLE OF INVENTION: Site Specific Nucleic Acid Integration  
: FILE REFERENCE: AVI-025CIP3  
: CURRENT APPLICATION NUMBER: US/10/940.315  
: CURRENT FILING DATE: 2004-09-14  
: NUMBER OF SEQ ID NOS: 13  
: SOFTWARE: PatentIn version 3.2  
: SEQ ID NO 10  
: LENGTH: 6233  
: TYPE: DNA  
: ORGANISM: Artificial Sequence  
: FEATURE:  
: OTHER INFORMATION: Plasmid PCR-XL-TORO-CMV-pur-ateb  
US-10-940-315-10

Query Match 30.9%; Score 1634.4; DB 8; Length 6233;  
Best Local Similarity 80.6%; Pred. No. 0;  
Matches 2082; Conservative 0; Mismatches 211; Indels 291; Gaps 3;

Qy 2942 CTTCCGCTTCTCGCTCACTGACTGCTGCGCTGCGTCTTCCGCTGCGGAGCCGTAT 3001  
Db 6233 CTTCCGCTTCTCGCTCACTGACTGCTGCGCTGCGTCTTCCGCTGCGGAGCCGTAT 6174  
Qy 3002 CAGCTCACTCAAGGCGGTATACGGTTATCCAGAGATCAGGGGATATACGAGAAAGA 3061  
Db 6173 CAGCTCACTCAAGGCGGTATACGGTTATCCAGAGATCAGGGGATATACGAGAAAGA 6114  
Qy 3062 ACATGTGACAAAGGCGGAGAAAGCCAGAAACCGTAAAGGCGCGTGTGCTGCGT 3121  
Db 6113 ACATGTGACAAAGGCGGAGAAAGCCAGAAACCGTAAAGGCGCGTGTGCTGCGT 6054  
Qy 3122 TTTTCATAGGCTCGGCCCCCTGACGAGCATCAAAAATCGACGCTCAAGTAGAGT 3181  
Db 6053 TTTTCATAGGCTCGGCCCCCTGACGAGCATCAAAAATCGACGCTCAAGTAGAGT 5994  
Qy 3182 GCGGAAACCCGACAGAGATATTAAGATACAGGCGTTCCCGCTGGAAGTCCCTCGTGC 3241  
Db 5993 GCGGAAACCCGACAGAGATATTAAGATACAGGCGTTCCCGCTGGAAGTCCCTCGTGC 5934  
Qy 3242 GCTCTCTGTTCCGACCCCTGCGCTTACCGGATACGTGTCCGCTTCTCCCTTGGGAA 3301  
Db 5933 GCTCTCTGTTCCGACCCCTGCGCTTACCGGATACGTGTCCGCTTCTCCCTTGGGAA 5874  
Qy 3302 GCGTGGCCTTCTCATAGCTCAAGCTGATAGTATCTAGTTCCGTGTAAGTCCGTGCT 3361  
Db 5873 GCGTGGCCTTCTCATAGCTCAAGCTGATAGTATCTAGTTCCGTGTAAGTCCGTGCT 5814  
Qy 3362 CCAAGCTGGGCTGTGTGACGAAACCCCGTTACGCGCCGACCGCTGCGCTTATCCGTA 3421  
Db 5813 CCAAGCTGGGCTGTGTGACGAAACCCCGTTACGCGCCGACCGCTGCGCTTATCCGTA 5754  
Qy 3422 ACTATGCTGTGAGTCCAAACCGGTAAAGACAGACTTATCGCACTGCGAGAGCACTG 3481  
Db 5753 ACTATGCTGTGAGTCCAAACCGGTAAAGACAGACTTATCGCACTGCGAGAGCACTG 5694  
Qy 3482 GTAAGAGATTAGCAGAGAGAGTATGTAGCGGAGTCAAGAGTTCTTGAAGTGGTGC 3541  
Db 5693 GTAAGAGATTAGCAGAGAGAGTATGTAGCGGAGTCAAGAGTTCTTGAAGTGGTGC 5634  
Qy 3542 CTAAGTACGGCTACACTAGAAAGAGATTTGTATCTGCGCTCTGTGAAGCCAGTTA 3601  
Db 3601

Db 5633 CTAAGTACGGCTACACTAGAAAGAGATTTTGTATCTGCGCTCTGTGAAGCCAGTTA 5574  
Qy 3602 CTTTCGAAAAAGATTGTAAGTCTTGTATTCGCGAAACCAACCGCTGTAGCGGTG 3661  
Db 5573 CTTTCGAAAAAGATTGTAAGTCTTGTATTCGCGAAACCAACCGCTGTAGCGGTG 5514  
Qy 3662 GTTTTTTGTGTCAGAGCAGAGATTAAGCGCAGAAAAAGGATCTCAAGAGATCTT 3721  
Db 5513 GTTTTTTGTGTCAGAGCAGAGATTAAGCGCAGAAAAAGGATCTCAAGAGATCTT 5454  
Qy 3722 TGATCTTTTCTACGGGCTGTGACGCTCAGTGGAGCAAAACTCAGCTTAAGGATTTTG 3781  
Db 5453 TGATCTTTTCTACGGGCTGTGACGCTCAGTGGAGCAAAACTCAGCTTAAGGATTTTG 5394  
Qy 3782 TCATGAGTTATC----- 3794  
Db 5393 TCATGAGTTATCAAAAAGATCTTCACTAGATCTTTTAATTAAATGAAGTTTAA 5334  
Qy 3795 -----GTCAGCA 3802  
Db 5333 GCAAGTGTACGTCGCTCTCTGCGCAGAAAGTGCAGAGTTCGCGCGCGGTGCGCA 5274  
Qy 3803 AAGCGGCATGCTGCTCTCCCACTCTGCAATTGCGGGCATGATGCGGGATAGCGGC 3862  
Db 5273 GGGCGAACTCCGCGCCCAAGGCTGCTCGCGATCTCGGTATGCGCGCGCGCGT 5214  
Qy 3863 TGCTGTCTTCTGATGCGCAGAGATTTGCACTGCGCGTGAACCTCCGAGAGTGTGCA 3922  
Db 5213 CCGGAAAGTTGTGACACAGACTCCGACACTCGGCGTACAGCTGTTCAGGCGCGCA 5154  
Qy 3923 GCC----- 3925  
Db 5153 CCAACACCAAGCAGAGTGTGTCCGCGACCAAGCTGCTTGAACCGCGCTGATGAACA 5094  
Qy 3926 ---TCAGGACAGCTGAACCAACTCGCGAGGAGTCAAGCTCGGAGTGGCGAAACT 3982  
Db 5093 GGGTCAAGTGTCCGCGACCAACCGCGAAGTGTCTCCACGAAATCCCGGAGAAC 5034  
Qy 3983 CAGCATGATATCCCGCGCTGAGAGATATCAAGCGCGCGTCCGGAAGAGATTCGA 4042  
Db 5033 CAGCGCGTGTGTCGAAACTGACCGCTCCGCGCAGTCCGCGCGGTGAGCACCGGAA 4974  
Qy 4043 AGCCCACTTTTCATGAAAGCGCGCGGTGAATCGAAATCTGTAATGCGAGTGGGCG 4102  
Db 4973 CCGCAGTGTCAACTTGGCATGTGTGCGCTCAGTGTATTTGAAGCATTTATC 4914  
Qy 4103 TCGCTTGTGCTCATTTTGAACCCGAGTCCG----- 4137  
Db 4913 AGGTTATTGTCTCATGAGCGGATACATATTGAATGTAATTAGAAAAATAACAATAG 4854  
Qy 4138 ----- 4137  
Db 4853 GGGTTCGCGCACATTTCCCGAAAGTGCCACCTGTATGCGGTGMAAATACCGCACAG 4794  
Qy 4138 -----CTCAGAGAACTC 4150  
Db 4793 ATGGTAAGGAGAAATATCCGCATCAGAAATTGTAAGCGTTAATTAATTCAGAAAGAACTC 4734  
Qy 4151 GTCAAGAGCGCATTAAGAGCGATGTGCTGCGAAATGCGGAGCGCGCATACCGTAAGCAC 4210  
Db 4733 GTCAAGAGCGCATTAAGAGCGATGTGCTGCGAAATGCGGAGCGCGCATACCGTAAGCAC 4674  
Qy 4211 GAGAGAGCGGTCAAGCCATTCGCGCAAGCTTTTCAAGAAATATCAAGGATGCAACG 4270  
Db 4673 GAGAGAGCGGTCAAGCCATTCGCGCAAGCTTTTCAAGAAATATCAAGGATGCAACG 4614  
Qy 4271 TATGCTCTGATTAAGCGGTCCGCAACCCAGCGGCAAGTGTATATTCAGAAAGG 4330  
Db 4613 TATGCTCTGATTAAGCGGTCCGCAACCCAGCGGCAAGTGTATATTCAGAAAGG 4554  
Qy 4331 GCCATTTTCCACCATGATATTTCCGCAAGCAGAGATGCCATGGGTACAGCGAGATCTTC 4390  
Db 4553 GCCATTTTCCACCATGATATTTCCGCAAGCAGAGATGCCATGGGTACAGCGAGATCTTC 4494





November 2005

Published\_Applications\_Nucleic Acid and Published\_Applications\_Amino Acid database searches now generate two sets of results each. The Published\_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Applications\_New databases; older published applications make up the Published\_Applications\_Main databases.

Searches run against Nucleic Acid Published\_Applications produce two sets of results, with the extensions **.rnpbn** (Published\_Applications\_NA\_Main) and **.rnpbn** (Published\_Applications\_NA\_New).

Searches run against Amino Acid Published\_Applications produce two sets of results, with the extensions

**.rapbn** (Published\_Applications\_AA\_Main) and **.rapbn** (Published\_Applications\_AA\_New).

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QY 181 ACGAGACTTCAAAATGTCGTAAACAATCGGCCCATTTGACGCAATGGCGGTAGGGC 240  
| | | | |  
Db 181 ACGAGACTTCAAAATGTCGTAAACAATCGGCCCATTTGACGCAATGGCGGTAGGGC 240  
QY 241 AACATGCTTAATGTAACGGTAGATTAGCAACATGCTTTATAGAGAGAAAAAGCACCGTG 300  
| | | | |  
Db 241 AACATGCTTAATGTAACGGTAGATTAGCAACATGCTTTATAGAGAGAAAAAGCACCGTG 300  
QY 301 CAGCGCATTTGGTGGAGTAAGGTGATGATCGTGGTATGATCGTGTCCCTTTGTAAGAG 360  
| | | | |  
Db 301 CAGCGCATTTGGTGGAGTAAGGTGATGATCGTGGTATGATCGTGTCCCTTTGTAAGAG 360  
QY 361 GCAACAGACGGGTCTAAACAGAGTTGGACGAACCACTGAATTCGCGATTGACAGATATT 420  
| | | | |  
Db 361 GCAACAGACGGGTCTAAACAGAGTTGGACGAACCACTGAATTCGCGATTGACAGATATT 420  
QY 421 GTAATTAAGTCCCAAGCTGATACAAATPAA CGCCATTGACAAATTCACCAATTGGTGTG 480  
| | | | |  
Db 421 GTAATTAAGTCCCAAGCTGATACAAATPAA CGCCATTGACAAATTCACCAATTGGTGTG 480  
QY 481 CACCTGGTGGATGATGATCAATCAATGCACTTCGTGGGCTTTCTCTGTGGGCTTCT 540  
| | | | |  
Db 481 CACCTGGTGGATGATGATCAATCAATGCACTTCGTGGGCTTTCTCTGTGGGCTTCT 540  
QY 541 CTGCTCGCGCTGCTGCTCCGGGCTCTCGCGAGGCGCCGCGCGCGCGCGCTTC 600  
| | | | |  
Db 541 CTGCTCGCGCTGCTGCTCCGGGCTCTCGCGAGGCGCCGCGCGCGCGCGCTTC 600  
QY 601 GAGTCGGGACTGCACTCTTCGGA CGCGGAGCCGGA CGCGGGTGAAGGCA CGGCTTAATGA 660  
| | | | |  
Db 601 GAGTCGGGACTGCACTCTTCGGA CGCGGAGCCGGA CGCGGGTGAAGGCA CGGCTTAATGA 660  
QY 661 AGCAAAATTTGAGAGGAGGATTAACGGTCTGTGCCAGTGAATGAATCAATGACTGTA 720  
| | | | |  
Db 661 AGCAAAATTTGAGAGGAGGATTAACGGTCTGTGCCAGTGAATGAATCAATGACTGTA 720  
QY 721 CTCTACCCAGAAATTTGAGAAATGTAACAATGTCAGCTAAGAAAGAGGCTGGCAAT 780  
| | | | |  
Db 721 CTCTACCCAGAAATTTGAGAAATGTAACAATGTCAGCTAAGAAAGAGGCTGGCAAT 780  
QY 781 AACAGAGACAGGCCCAACTCTCAACTCAAGGACAGAAAGACTTAATAATTTGCTGACGA 840  
| | | | |  
Db 781 AACAGAGACAGGCCCAACTCTCAACTCAAGGACAGAAAGACTTAATAATTTGCTGACGA 840  
QY 841 CATTATTAATCAAGATCTTGAAAGATGATGAATGAATGAGGAAAGACTTCATGATG 900  
| | | | |  
Db 841 CATTATTAATCAAGATCTTGAAAGATGATGAATGAATGAGGAAAGACTTCATGATG 900  
QY 901 CCAAGGAGGTGTGTATAGATGTGGGAGAGAGTTTGGAGTCCGCAAAACCTTCTTT 960  
| | | | |  
Db 901 CCAAGGAGGTGTGTATAGATGTGGGAGAGAGTTTGGAGTCCGCAAAACCTTCTTT 960  
QY 961 AAACCTTCATGTGTGCTGCTCAAGATGTGGGGGTTGCTGCATAATGTAAGGGCTGACG 1020  
| | | | |  
Db 961 AAACCTTCATGTGTGCTGCTCAAGATGTGGGGGTTGCTGCATAATGTAAGGGCTGACG 1020  
QY 1021 TGCATGAACACAGCA CGAGCTACCTCAGCAAGACGTTATTTGAAATTAAGTGCCCTTC 1080  
| | | | |  
Db 1021 TGCATGAACACAGCA CGAGCTACCTCAGCAAGACGTTATTTGAAATTAAGTGCCCTTC 1080  
QY 1081 TCTCAAGGCCCCCAACAGATCAATCAATGATTTGCAATCACTTCCTGCAATGATG 1140  
| | | | |  
Db 1081 TCTCAAGGCCCCCAACAGATCAATCAATGATTTGCAATCACTTCCTGCAATGATG 1140  
QY 1141 TCTTAACTGATGTTTACAGACAAATTCATTAATTAAGACGTTCCCTGACAGACA 1200  
| | | | |  
Db 1141 TCTTAACTGATGTTTACAGACAAATTCATTAATTAAGACGTTCCCTGACAGACA 1200  
QY 1201 CTACCAAGGTGATGAGGAGGCAACAGACTGCGCCCACTTAATTAATGATTAATC 1260  
| | | | |  
Db 1201 CTACCAAGGTGATGAGGAGGCAACAGACTGCGCCCACTTAATTAATGATTAATC 1260

QY 1261 ATCTGAGATGCTGGGCTCAGAAAGATTTATGTTTTTCCCGGATGCTGAGATGACTCA 1320  
| | | | |  
Db 1261 ATCTGAGATGCTGGGCTCAGAAAGATTTATGTTTTTCCCGGATGCTGAGATGACTCA 1320  
QY 1321 ACAGATGATTCCTCANTGACATCTGTGACCAACAGAGAGCTGATGAAGACCTGTGAG 1380  
| | | | |  
Db 1321 ACAGATGATTCCTCANTGACATCTGTGACCAACAGAGAGCTGATGAAGACCTGTGAG 1380  
QY 1381 TGTGTCTGACAGAGCGGGGCTTCGGCTTCGACAGTGTGAGACCCCAAGAAACTGACAGA 1440  
| | | | |  
Db 1381 TGTGTCTGACAGAGCGGGGCTTCGGCTTCGACAGTGTGAGACCCCAAGAAACTGACAGA 1440  
QY 1441 AACTCATGCAAGTGTCTGTATAAAACAAACTTTCCTCCAGCCCAATGTGGGGCCAAACGA 1500  
| | | | |  
Db 1441 AACTCATGCAAGTGTGTGTATAAAACAAACTTTCCTCCAGCCCAATGTGGGGCCAAACGA 1500  
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| | | | |  
Db 1501 GAAATTTGATGAAAACATGCGAGTGTATGTAAGAAAGAACTGCCCCAGAAATCAACCC 1560  
QY 1561 CTAATTCCTGGAAAATGTGCTGTGAAATGTAAGAAAGTCCACAGAAATGCTTTTAAAA 1620  
| | | | |  
Db 1561 CTAATTCCTGGAAAATGTGCTGTGAAATGTAAGAAAGTCCACAGAAATGCTTTTAAAA 1620  
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| | | | |  
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QY 1681 AAGCTTGTGAGCGCAGGATTTTCAATPAGTGAAGAGTGTGTGTTGCTTCAATAT 1740  
| | | | |  
Db 1681 AAGCTTGTGAGCGCAGGATTTTCAATPAGTGAAGAGTGTGTGTTGCTTCAATAT 1740  
QY 1741 TGGAAAAGACCAAAATGAGCTTAATCTAGGATCCGTAACCTGCGCAGGCTTTTGTCAAC 1800  
| | | | |  
Db 1741 TGGAAAAGACCAAAATGAGCTTAATCTAGGATCCGTAACCTGCGCAGGCTTTTGTCAAC 1800  
QY 1801 AGCACTTTGTGTTCTCACTTGTGGAAGCTCTCACTGAGTGTGGGAGCGTGGAT 1860  
| | | | |  
Db 1801 AGCACTTTGTGTTCTCACTTGTGGAAGCTCTCACTGAGTGTGGGAGCGTGGAT 1860  
QY 1861 TCTTCTACACACCATGTCCTCCGCGGAAGTGAAGACCAAGGTAAGCTTCGCTCCT 1920  
| | | | |  
Db 1861 TCTTCTACACACCATGTCCTCCGCGGAAGTGAAGACCAAGGTAAGCTTCGCTCCT 1920  
QY 1921 GAATTCATCCCAAGGCTTAATCACTGTTGTCTTCACTTGAAGCTTTGTAATTT 1980  
| | | | |  
Db 1921 GAATTCATCCCAAGGCTTAATCACTGTTGTCTTCACTTGAAGCTTTGTAATTT 1980  
QY 1981 GTGCCCTAGGTGTGAGGGTCTCAGGCTTAACAGTGGGGGCACTTTCTGTGGGAGCT 2040  
| | | | |  
Db 1981 GTGCCCTAGGTGTGAGGGTCTCAGGCTTAACAGTGGGGGCACTTTCTGTGGGAGCT 2040  
QY 2041 AGCATATGTAACATGTGATGCTGCCAGAGAGAGTGAATCTTTCCTTAAGTCTCTA 2100  
| | | | |  
Db 2041 AGCATATGTAACATGTGATGCTGCCAGAGAGAGTGAATCTTTCCTTAAGTCTCTA 2100  
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| | | | |  
Db 2101 GGTGTGAGAGGGGTGCTAAGGCCCAAGATAGGATCTAATTTGGGGACCCCATGAGACCT 2160  
QY 2161 GCACTGACTGAGGGATGATGAAGATGTATGATTTTGAAGGCCCATATGTCATTTCAAT 2220  
| | | | |  
Db 2161 GCACTGACTGAGGGATGATGAAGATGTATGATTTTGAAGGCCCATATGTCATTTCAAT 2220  
QY 2221 GACCACTGACTGTCTCAAGCCATGCAACCTTGTCTCTGTGTGACTTGAAGAGGGA 2280  
| | | | |  
Db 2221 GACCACTGACTGTCTCAAGCCATGCAACCTTGTCTCTGTGTGACTTGAAGAGGGA 2280  
QY 2281 TAAAGTGAAGAAAGCTGGGCTAATCAAGGGGTGCTAGGCTCCCTTAACGATGAT 2340  
| | | | |  
Db 2281 TAAAGTGAAGAAAGCTGGGCTAATCAAGGGGTGCTAGGCTCCCTTAACGATGAT 2340  
QY 2341 CCTATGTGTCTTGTGCTGTGTGATGCTGTGCTGCTGTGCTGATGACTTCCTG 2400  
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Dp	2341	CCTATGTGCTTTTGGCTTCTGTCTCTGTATGCTCTGCTGTGCTGATGACATGACCTTCCTG	2400
Qy	2401	GCAGTGGCACAATCGAGCTGGGTGGAGGCCCGGGGGGCAAGTACCTTCAGACTTTGGCA	2460
Dp	2401	GCAGTGGCACAATCGAGCTGGGTGGAGGCCCGGGGGGCAAGTACCTTCAGACTTTGGCA	2460
Qy	2461	CTGGAGGTGGCCCCGGGCAAGAGCGGGCATCTGTGATCTAGTGTGCAACGACATCTGCTCT	2520
Dp	2461	CTGGAGGTGGCCCCGGGCAAGAGCGGGCATCTGTGATCTAGTGTGCAACGACATCTGCTCT	2520
Qy	2521	CTCTACCAACTGGAGAACTACTGCAACTAGAGCCCACTACCCGTGCACCCCTGTGCA	2580
Dp	2521	CTCTACCAACTGGAGAACTACTGCAACTAGAGCCCACTACCCGTGTCAACCCCTGTGCA	2580
Qy	2581	ATGAATAAAACTTTGAAAGAGCACTACAAGTTGTGTATCATGCGTCATGTGCATATG	2640
Dp	2581	ATGAATAAAACTTTGAAAGAGCACTACAAGTTGTGTATCATGCGTCATGTGCATATG	2640
Qy	2641	TGCTGCGGGGGGGAACATGATGTGGGCTGGCTGGAGTGTTCGGGCTTAATCTATCTGCA	2700
Dp	2641	TGCTGCGGGGGGGAACATGATGTGGGCTGGCTGGAGTGTTCGGGCTTAATCTATCTGCA	2700
Qy	2701	GCTGTCTAGACGTATCATAGGTCATAGCGTTTCCGTGTGTAATAATGTTATCCGCTACA	2760
Dp	2701	GCTGTCTAGACGTATCATAGGTCATAGCGTTTCCGTGTGTAATAATGTTATCCGCTACA	2760
Qy	2761	ATTCCACAACAATACGAGCCGGAAGCACTAAAGTCTAAAGCTGGGGGCGCTTAATGATG	2820
Dp	2761	ATTCCACAACAATACGAGCCGGAAGCACTAAAGTCTAAAGCTGGGGGCGCTTAATGATG	2820
Qy	2821	AGCTAACTCACTAATTAATTCGTTGGCTCACTGCCCGCTTTCAGTCGGGAAACCTGTG	2880
Dp	2821	AGCTAACTCACTAATTAATTCGTTGGCTCACTGCCCGCTTTCAGTCGGGAAACCTGTG	2880
Qy	2881	TGCCAGCTGCATTTATGAAATGGGCCAAGCGCGGGGAAAGCGGTTTCCGTAATGGCGGC	2940
Dp	2881	TGCCAGCTGCATTTATGAAATGGGCCAAGCGCGGGGAAAGCGGTTTCCGTAATGGCGGC	2940
Qy	2941	TCTTCGCTTCCTCGCTCACTGACTCGCTGGGCTCGGTGTTCCGCTGCGCGAGCCGTA	3000
Dp	2941	TCTTCGCTTCCTCGCTCACTGACTCGCTGGGCTCGGTGTTCCGCTGCGCGAGCCGTA	3000
Qy	3001	TCAGCTCACTCAAAAGCGGTAAATACGGTTATCCACAGAACTACGGGGAATACCGAGAAAG	3060
Dp	3001	TCAGCTCACTCAAAAGCGGTAAATACGGTTATCCACAGAACTACGGGGAATACCGAGAAAG	3060
Qy	3061	AACATGTGAGCAAAAAGGCCAGCAAAAAGGCCAGAAACGTTAAAAAAGCGCTGTGGCG	3120
Dp	3061	AACATGTGAGCAAAAAGGCCAGCAAAAAGGCCAGAAACGTTAAAAAAGCGCTGTGGCG	3120
Qy	3121	TTTTTCCATAGAGCTCCGGCCCCCGTGAAGAGATCAAAAATTCGACGTCGAAGTCAGAG	3180
Dp	3121	TTTTTCCATAGAGCTCCGGCCCCCGTGAAGAGATCAAAAATTCGACGTCGAAGTCAGAG	3180
Qy	3181	TGGGAAACCAGAGAGACTAATAAGATACAGAGCGTTCCCTCTGAGAGTCTCCTGCT	3240
Dp	3181	TGGGAAACCAGAGAGACTAATAAGATACAGAGCGTTCCCTCTGAGAGTCTCCTGCT	3240
Qy	3241	CGCTCTCTGTTCCGACCTTCGCGCTTACCGGATACCTGTCCGCTTTCCTTCGGGA	3300
Dp	3241	CGCTCTCTGTTCCGACCTTCGCGCTTACCGGATACCTGTCCGCTTTCCTTCGGGA	3300
Qy	3301	AGCGGGGCGCTTTCATAGCTCAACGCTGATAGATCTCAATTCGAGTGTAGTGTGCTCGC	3360
Dp	3301	AGCGGGGCGCTTTCATAGCTCAACGCTGATAGATCTCAATTCGAGTGTAGTGTGCTCGC	3360
Qy	3361	TCCAAGCTGGGCTGTGTGCAAGAACCCCGCTTACGCCCAACCGCTGCTTATCCGCT	3420
Dp	3361	TCCAAGCTGGGCTGTGTGCAAGAACCCCGCTTACGCCCAACCGCTGCTTATCCGCT	3420
Qy	3421	AACATGTGCTTTGAGTCCAAACCCGGTAAGACAGACTTATGCGCACTTGGCAGACCACT	3480
Dp	3421	AACATGTGCTTTGAGTCCAAACCCGGTAAGACAGACTTATGCGCACTTGGCAGACCACT	3480

Db	3421	AACTATCGTCTTGAAGTCCAAACCCGGTAAAGACAGCACTTATGCCACTGGACAGCAACT	3481
Qy	3481	GGTAAACAGATTATGACAGACGAGTATGAGCGGTGTGTACAGATTCTTGAATGTGTGG	3541
Db	3481	GGTAAACAGATTATGACAGACGAGTATGTAAGCGGTGTGTACAGATTCTTGAATGTGTGG	3541
Qy	3541	CCTAACTACGGCTACACTAGAAAGAACAGTATTTGGTATCTGGCGCTCTGCTGAAGCACTT	3601
Db	3541	CCTAACTACGGCTACACTAGAAAGAACAGTATTTGGTATCTGGCGCTCTGCTGAAGCACTT	3601
Qy	3601	ACCTTCGGAAAAAGTGGTATAGCTCTGATCCGGCAAAACAACCGCTGTGTAGCGGT	3661
Db	3601	ACCTTCGGAAAAAGTGGTATAGCTCTGATCCGGCAAAACAACCGCTGTGTAGCGGT	3661
Qy	3661	GGTTTTTTTGGTTTGGACAGACAGATTATCGCGCAGAAAAAAGATCTCAAGAAAGATCTT	3721
Db	3661	GGTTTTTTTGGTTTGGACAGACAGATTATCGCGCAGAAAAAAGATCTCAAGAAAGATCTT	3721
Qy	3721	TTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAAGAAAACTCAGTTAAGGATTTTG	3781
Db	3721	TTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAAGAAAACTCAGTTAAGGATTTTG	3781
Qy	3781	GTCATGAAATATATCGTCCAGCAACCAAGCGGCCATCGTGCTCCCCACTCTGCAAGTTCCGGG	3841
Db	3781	GTCATGAAATATATCGTCCAGCAACCAAGCGGCCATCGTGCTCCCCACTCTGCAAGTTCCGGG	3841
Qy	3841	GCATGATGACCGCGGATACCGCTGCTGGTTTCTGGAATGCCAGACGGAATTTGCACTTCCGGG	3901
Db	3841	GCATGATGACCGCGGATACCGCTGCTGGTTTCTGGAATGCCAGACGGAATTTGCACTTCCGGG	3901
Qy	3901	TAGAACTCCGCGAGGTGCTCCAGCTCCAGGACGAGCTGAACCACTTCGACGAGGGAGATCG	3961
Db	3901	TAGAACTCCGCGAGGTGCTCCAGCTCCAGGACGAGCTGAACCACTTCGACGAGGGAGATCG	3961
Qy	3961	AGCCCGGGGGTGGGCGGAAGAACTCCAGCATAGATATCCCGCGCTGAGAGATATCCAGCG	4021
Db	3961	AGCCCGGGGGTGGGCGGAAGAACTCCAGCATAGATATCCCGCGCTGAGAGATATCCAGCG	4021
Qy	4021	GCATCCCGGAAAAAGATTCGGAAGCGCAACCTTTCATAGAAAGGGCGGTGGAATTCGAAA	4081
Db	4021	GCATCCCGGAAAAAGATTCGGAAGCGCAACCTTTCATAGAAAGGGCGGTGGAATTCGAAA	4081
Qy	4081	TCTCGTAGTAGCAGATTGGGCGTGCCTTGATCGGTCAATTTGAAACCCAGAGTCCCGCTC	4141
Db	4081	TCTCGTAGTAGCAGATTGGGCGTGCCTTGATCGGTCAATTTGAAACCCAGAGTCCCGCTC	4141
Qy	4141	AGAAAGAACTCGTCAAGAAAGGCGATAGAAAGGCGATGCGCTGGAATCCGGAACCGCGCATAC	4201
Db	4141	AGAAAGAACTCGTCAAGAAAGGCGATAGAAAGGCGATGCGCTGGAATCCGGAACCGCGCATAC	4201
Qy	4201	CGTAAAGACGAGGAAGCGGTCAACCCATTCCGCGCAAGCTCTTCAGCAATATCAACGGG	4261
Db	4201	CGTAAAGACGAGGAAGCGGTCAACCCATTCCGCGCAAGCTCTTCAGCAATATCAACGGG	4261
Qy	4261	TAGCCAAACGCTATATCTCGATAGAGGATCCGCAACCCAGCGCGCAACAGTCATGATATC	4321
Db	4261	TAGCCAAACGCTATATCTCGATAGAGGATCCGCAACCCAGCGCGCAACAGTCATGATATC	4321
Qy	4321	CAGAAAAACGGCCATTTTCCACCATGATATTCGGCAAGCAGGCAATCGCATGGGTACGA	4381
Db	4321	CAGAAAAACGGCCATTTTCCACCATGATATTCGGCAAGCAGGCAATCGCATGGGTACGA	4381
Qy	4381	CGAATATCTCGCGCTCGGGGCAATGGGCGCTTTGAGACCTGGGGAACAGTTTCGGCTGGCGCA	4441
Db	4381	CGAATATCTCGCGCTCGGGGCAATGGGCGCTTTGAGACCTGGGGAACAGTTTCGGCTGGCGCA	4441
Qy	4441	GGCCCTGATGCTCTTCGTCAGATCACTCGATGGAACAACCGGCTTCCATCCGATAC	4501
Db	4441	GGCCCTGATGCTCTTCGTCAGATCACTCGATGGAACAACCGGCTTCCATCCGATAC	4501
Qy	4501	GTCGTCGCTCGATGCGATGTTTGGCTTGATGGTGAATGGGCAAGTAGCCGAATCAAGCG	4561
Db	4501	GTCGTCGCTCGATGCGATGTTTGGCTTGATGGTGAATGGGCAAGTAGCCGAATCAAGCG	4561



QY 3863 TGCTGTTTCTTGATCCGACGATTTTGCATCTGCGGTGAGAACTCCGCGAGTGTCTCA 3922  
 DB 4205 CCCGGAAGTTGTGGAACACGACCTCCGACCACTGGGCTTACAGCTCTGTCAGGCGCGCA 4146  
 QY 3923 GCC----- 3925  
 DB 4145 CCCACACCCAGGCGAGGTGTGTTCGCGCACCTGGTCTTGGACGCGCTGATGAACA 4086  
 QY 3926 ---TCAGGACAGCTGTAACCACTCGGAGGGGATGAGCCGGGGTGGCGGAAGACT 3982  
 DB 4085 GGGTCAAGTGTCTCCGACACACCGGGAGTGTCTTCCACAGAAATCCGGGAGAAC 4026  
 QY 3983 CCAGCATG-----AGATCCCGCGCTGAGAGATCATCCAGCGCGCTC 4025  
 DB 4025 CGAGCTGTGCACTTGGCCCATGTGGGCCCTCTCACTGCTATATTAGAAACATTTATC 3966  
 QY 4026 CCGGAAAACATTTCCGAAGCCCACTTTCAATAGAAAGCGGGGTGAATCGAAATCTCG 4085  
 DB 3965 AGGGTTATTGTCTCATGAGCGGATATATTGATGATTTAGAAAAATAAACAATAG 3906  
 QY 4086 TGAATGAGGTTGGGCGTCCGTTGTGCTGATTTCCAGCCGAGATCCCGC----- 4138  
 DB 3905 GGGTTCCGCGCAATTTCCCGAAAAGTCCACTGTATGCGGTGAAAATACGCAAG 3846  
 QY 4139 -----TCAGAAACTC 4150  
 DB 3845 ATGCGTAAGGAGAAATACCGCATCAGAAATTTGTAACGTTAATTCAGAAACTC 3786  
 QY 4151 GTCAGAAAGCGGATAGAAAGCGGATGCGCTGCGAATCGGAGCGGCGATACCGTAAAGCAC 4210  
 DB 3785 GTCAGAAAGCGGATAGAAAGCGGATGCGCTGCGAATCGGAGCGGCGATACCGTAAAGCAC 3726  
 QY 4211 GAGGAAAGCGGATAGAAAGCGGATGCGCTGCGAATCGGAGCGGCGATACCGTAAAGCAC 4270  
 DB 3725 GAGGAAAGCGGATAGAAAGCGGATGCGCTGCGAATCGGAGCGGCGATACCGTAAAGCAC 3666  
 QY 4271 TATGCTGATAGAGGCTCCGACACCGAGCGGCGCAAGTCATGATCAGAAAGCG 4330  
 DB 3665 TATGCTGATAGAGGCTCCGACACCGAGCGGCGCAAGTCATGATCAGAAAGCG 3606  
 QY 4331 GCCATTTTCACCATGATATTTGGCAAGGACATCCCATGGGTCAAGAGATCTTC 4390  
 DB 3605 GCCATTTTCACCATGATATTTGGCAAGGACATCCCATGGGTCAAGAGATCTTC 3566  
 QY 4391 GCGGTGGGATAGCGGCTTTGAGCTGGGGAAGATTTGGCTGGCGGAGCCCTGATG 4450  
 DB 3545 GCGGTGGGATAGCGGCTTTGAGCTGGGGAAGATTTGGCTGGCGGAGCCCTGATG 3486  
 QY 4451 CTCTTGGTCAGATCATCTGATCGACAGACCGGCTTCATCCGATAGTGTGCTC 4510  
 DB 3485 CTCTTGGTCAGATCATCTGATCGACAGACCGGCTTCATCCGATAGTGTGCTC 3426  
 QY 4511 GATGCGATGTTTGGCTTGTGTCGATGGAATGGGAGTAGCCGATCAAGCTATGACCG 4570  
 DB 3425 GATGCGATGTTTGGCTTGTGTCGATGGAATGGGAGTAGCCGATCAAGCTATGACCG 3366  
 QY 4571 CCGCATTTGCATCAGCCATGATGATCTTTCTGGCGAGGCAAGGTGAGATGACGAG 4630  
 DB 3365 CCGCATTTGCATCAGCCATGATGATCTTTCTGGCGAGGCAAGGTGAGATGACGAG 3306  
 QY 4631 ATCTGCGCGGACATTTGCGCAATAGCAGCAGTCCCTTCGCGCTTCACTGACAACTC 4690  
 DB 3305 ATCTGCGCGGACATTTGCGCAATAGCAGCAGTCCCTTCGCGCTTCACTGACAACTC 3246  
 QY 4691 GAGCAGAGCTGCGCAAGGAGCGCCGCTGTGGCAGCCAGATAGCCGCTGCTGTC 4750  
 DB 3245 GAGCAGAGCTGCGCAAGGAGCGCCGCTGTGGCAGCCAGATAGCCGCTGCTGTC 3186  
 QY 4751 CTGCAATTTTCAAGGCAACCGGACAGAGTGGTCTTGAACAAAAAGAACCGGGGCGCTG 4810  
 DB 3185 TTGCAATTTTCAAGGCAACCGGACAGAGTGGTCTTGAACAAAAAGAACCGGGGCGCTG 3126

QY 4811 CGTGAAGCCGGAACACGCGCGCATCAGACAGCCGATTTGTGTTGCGCAGTCA 4870  
 DB 3125 CGTGAAGCCGGAACACGCGCGCATCAGACAGCCGATTTGTGTTGCGCAGTCA 3066  
 QY 4871 GCCGAATAGCCTCTCCACCCAGCGGCGGAGAACTGCGTGAATCCATCTTGTCAAT 4930  
 DB 3065 GCCGAATAGCCTCTCCACCCAGCGGCGGAGAACTGCGTGAATCCATCTTGTCAAT 3006  
 QY 4931 CATTGCGAAAGATCTCTCATCTGCTCTTGTATGATCTTGAATCCCTGCGCATTCAGAT 4990  
 DB 3005 CATTGCGAAAGATCTCTCATCTGCTCTTGTATGATCTTGAATCCCTGCGCATTCAGAT 2946  
 QY 4991 CTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGACAGGCTTCCCACTTAACAGAGG 5050  
 DB 2945 CTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGACAGGCTTCCCACTTAACAGAGG 2886  
 QY 5051 CGCCCAAGCTGGCAATTCGCGTTCGTTGCTGTCATTAACCGCCAGTCTAGCTATCG 5110  
 DB 2885 CGCCCAAGCTGGCAATTCGCGTTCGTTGCTGTCATTAACCGCCAGTCTAGCTATCG 2826  
 QY 5111 CCAATGAAGCCCACTGCAAGCTACTGCTTTCTTTGCGCTTGGCTTTCCCTGTGCA 5170  
 DB 2825 CCAATGAAGCCCACTGCAAGCTACTGCTTTCTTTGCGCTTGGCTTTCCCTGTGCA 2766  
 QY 5171 GATGAGCCAGTGAAGCTCATTCAGGAGTCAAGCAAGTTTCTGCGGAGTGGCTTCTA 5230  
 DB 2765 GATGAGCCAGTGAAGCTCATTCAGGAGTCAAGCAAGTTTCTGCGGAGTGGCTTCTA 2706  
 QY 5231 CGTG 5234  
 DB 2705 CGTG 2702

RESULT 3  
 US-10-517-698-1/c  
 ; Sequence 1, Application US/10517698  
 ; Publication No. US20060068390A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tiller et al.  
 ; TITLE OF INVENTION: DNA AMPLIFICATION AND SEQUENCING IN COLLAPSIBLE EMULSIONS  
 ; FILE REFERENCE: 23004/40746  
 ; CURRENT APPLICATION NUMBER: US/10/517,698  
 ; CURRENT FILING DATE: 2004-12-13  
 ; PRIORITY APPLICATION NUMBER: PCT/AU03/00746  
 ; PRIORITY FILING DATE: 2003-06-13  
 ; PRIOR APPLICATION NUMBER: AU PS 2981  
 ; NUMBER OF SEQ ID NOS: 11  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 1  
 ; LENGTH: 4245  
 ; TYPE: DNA  
 ; ORGANISM: Artificial sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Plasmid pCR-BIunt II-TOPO  
 US-10-517-698-1

Query Match 30.9%; Score 1634.4; DB 13; Length 4245;  
 Best Local Similarity 80.6%; Pred. No. 0;  
 Matches 2082; Conservative 0; Mismatches 211; Indels 291; Gaps 3;

QY 2942 CTTCCGCTTCTGCTCACTGATCGCTGCGCTGCTTGGCTGGCGGAGCGGTAT 3001  
 DB 4245 CTTCCGCTTCTGCTCACTGATCGCTGCGCTGCGCTTGGCTGGCGGAGCGGTAT 4186  
 QY 3002 CAGCTCACTCAAGGCGGTATACGTTATCCACAGATCAAGGAGATTAACGAGAAAG 3061  
 DB 4185 CAGCTCACTCAAGGCGGTATACGTTATCCACAGATCAAGGAGATTAACGAGAAAG 4126  
 QY 3062 ACATGTGACAAAGGCGCAGCAAAAGCCAGAAACGTTAAAGGCGCGTGTGCGCT 3121  
 DB 4125 ACATGTGACAAAGGCGCAGCAAAAGCCAGAAACGTTAAAGGCGCGTGTGCGCT 4066

QY	3122	TTTTTCATAGSGCTCGCCCCCTCTGACGACATCACAAAATCGACGCTCAAGTCAAGGT	3181
Db	4065	TTTTTCATAGSGCTCGCCCCCTCTGACGACATCACAAAATCGACGCTCAAGTCAAGGT	4006
QY	3182	GGCCGAACCCCGACAGGACCTAATAAGATACGAGGGTTTCCCTCGGAAGCTCCCGCGC	3241
Db	4005	GGCCGAACCCCGACAGGACCTAATAAGATACGAGGGTTTCCCTCGGAAGCTCCCGCGC	3946
QY	3242	GCTCTCTGTTCGACCCCTGCGGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGAAA	3301
Db	3945	GCTCTCTGTTCGACCCCTGCGGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGAAA	3886
QY	3302	GCGTGGCGCTTTCTATATAGCTACGCTGTAGGTATCTAAGTTCCGTGTAGGTCTGTGCT	3361
Db	3885	GCGTGGCGCTTTCTATATAGCTACGCTGTAGGTATCTAAGTTCCGTGTAGGTCTGTGCT	3826
QY	3362	CCAACTGGGCGTGTGTGACGACCCCGGTTACGCGGACCGCGTGGGCGCTTATCCGGTA	3421
Db	3825	CCAACTGGGCGTGTGTGACGACCCCGGTTACGCGGACCGCGTGGGCGCTTATCCGGTA	3766
QY	3422	ACTATCGTCTGAGTCCAAACCCGCTAAGACACGACTTATCCGCACTGCGACAGCACTG	3481
Db	3765	ACTATCGTCTGAGTCCAAACCCGCTAAGACACGACTTATCCGCACTGCGACAGCACTG	3706
QY	3482	GTAACAGGATTAGCAGACGACGAGGTATGTAGGCGGTCTACAGAGTTCTTGAAGTGTGTGC	3541
Db	3705	GTAACAGGATTAGCAGACGACGAGGTATGTAGGCGGTCTACAGAGTTCTTGAAGTGTGTGC	3646
QY	3542	CTAATCAGGCTACACTGTAGGAACAGATTTTGGATTTGGCGTCTGTGTGAAGCAGTTA	3601
Db	3645	CTAATCAGGCTACACTGTAGGAACAGATTTTGGATTTGGCGTCTGTGTGAAGCAGTTA	3586
QY	3602	CCTTTCGAAAAAAGAGTTGTGTAGCTCTTATCCGCAACAAACACGCTGTAGCGGTG	3661
Db	3585	CCTTTCGAAAAAAGAGTTGTGTAGCTCTTATCCGCAACAAACACGCTGTAGCGGTG	3526
QY	3662	GTTTTTTTGTTCGACGACGAGATTTACGCGCAGAAAAAAAGATCTTCAAGAGATCTT	3721
Db	3525	GTTTTTTTGTTCGACGACGAGATTTACGCGCAGAAAAAAAGATCTTCAAGAGATCTT	3466
QY	3722	TGATCTTTTTCACGGGGGTCTGACGCTCAGTGGAAACGAAACTCACGTTAAGGATTTTGG	3781
Db	3465	TGATCTTTTTCACGGGGGTCTGACGCTCAGTGGAAACGAAACTCACGTTAAGGATTTTGG	3406
QY	3782	TCATGAGATTAT-----	3794
Db	3405	TCATGAGATTATCAAAAAGATCTTACACTAGATCTTTTAAATTAATAATGAAGTTTTA	3346
QY	3795	-----GTTCGACA	3802
Db	3345	GCAAGTGTCAAGTCTGCTCTCTCGGCAAGAAGTGACGACAGTTGCGCGCGGTCGGCA	3286
QY	3803	AAGCGGCATGTGTGCTCTCCCACTCTCTGCAAGTTGGGGGCATGTGATGCGCGGATGCGCC	3862
Db	3285	AAGCGGCATGTGTGCTCTCCCACTCTCTGCAAGTTGGGGGCATGTGATGCGCGGCGGCGGCGT	3226
QY	3863	TGCTGTGTTCTGTGATGCGCAGATTTGCACTGCGCGGTAGAACCTCCGCGAGTCTGTCCA	3922
Db	3225	CCCGGAAGTTGATGAGACGACCTCCGACCACTCGGCGTACAGCTCTGTCCAGGCGCGCA	3166
QY	3923	GCC-----	3925
Db	3165	CCCAACACCAAGGCAAGGTGTTGTTCGGGCAACAAGTGTCTGTGACCGCGGTGATGAACA	3106
QY	3926	---TCAGCAGACGTGAACCACTTCGGAAGGAGTGAAGCCCGGAGTGGCGAAGAACT	3982
Db	3105	GGGTCAAGTCTGCTCCGGAACACACCGGGAAGTCTCTCCACAGAAAGTCCGGAAGAAC	3046
QY	3983	CCAGCATAGATCCCGGCGTGGAGAGATCATTCAGCGCGGCGCTCCCGAAGAACATTCGCA	4042
Db	3045	CGAGCGGATCGGTCCAGAACTTGACCGCTCCGGGCAAGTCCGCGCGGTGTGACACCGGAA	2986
QY	4043	AGCCCAACCTTTCATAGAAAGCGCGGTGGAATCGAAATCTGTGATGCGAGTTGGGCG	4102

Db	2985	CGGCACTGGTCAACTTGGCCATGGATGGCCCTCTCACGTGCTATTATTGAAGCATTTATC	2926
OY	4103	TGCGTTGGTCCGTCATTTCGAAATCCCAAGAGTCCG-----	4137
Db	2925	AGGGTATTGTCTCATGAGCGGATACATATTTGAATGATTATTAGAAAAATTAACAATAG	2866
OY	4138	-----	4137
Db	2865	GGGTTCCGCGACATTTCCCGAAAAAGTGCACCTGTATCGGCTGTGAAATATACGCACAG	2806
OY	4138	-----CTGAGAAATCTC	4150
Db	2805	ATGCGTAAAGAGAAATATCCGCATCAGGAAATTGTAAAGCTTAATTAATTCAGAAAGACTC	2746
OY	4151	GTCAAGAAAGCGATAGAAAGGCGATGCGCTGGATTCGGAGCGGCGAGATCCGTAAAGAC	4210
Db	2745	GTCAAGAAAGCGATAGAAAGCGATGCGCTGGATTCGGAGCGGCGAGATCCGTAAAGAC	2686
OY	4211	GAGAAAGCGGTCAAGCCCATTCGCGCCCAAGCTCTTCAGCAATATCAGGGATGACCAAGC	4270
Db	2685	GAGAAAGCGGTCAAGCCCATTCGCGCCCAAGCTCTTCAGCAATATCAGGGATGACCAAGC	2626
OY	4271	TATGTCTGATAGCGGTTCGCGCAACCAAGCGGCGCACAGTCTATGAAATCCAGAAAAAGC	4330
Db	2625	TATGTCTGATAGCGGTTCGCGCAACCAAGCGGCGCACAGTCTATGAAATCCAGAAAAAGC	2566
OY	4331	GCATATTTCCACATGATTAATTCGGCAAGCAGGATTCGCATGGGTCAAGCAGATCTCT	4390
Db	2565	GCATATTTCCACATGATTAATTCGGCAAGCAGGATTCGCATGGGTCAAGCAGATCTCT	2506
OY	4391	GCCTGCGGCGCATGCGCGCTTGAAGCTTGGCGAACAATTCCGCTGGCGGAGCCCTGTATG	4450
Db	2505	GCCTGCGGCGCATGCTCGCTTGAAGCTTGGCGAACAATTCCGCTGGCGGAGCCCTGTATG	2446
OY	4451	CTCTTTCGTCAGATCATCTGATGACAAAGCCGGCTTCCATCCGAGTACGTGCTCGCTC	4510
Db	2445	CTCTTTCGTCAGATCATCTGATGACAAAGCCGGCTTCCATCCGAGTACGTGCTCGCTC	2386
OY	4511	GATGCGATGTTTCCGTTGGTGTGTGAATGGGACAGTATGCGGATCAAGCGTATGACGCG	4570
Db	2385	GATGCGATGTTTCCGTTGGTGTGTGAATGGGACAGTATGCGGATCAAGCGTATGACGCG	2326
OY	4571	CCGATTCGCATCAGCCATGATGATGACTTCTCCGACAGAGCAAGGTGAGATGACAGAG	4630
Db	2325	CCGATTCGCATCAGCCATGATGATGACTTCTCCGACAGAGCAAGGTGAGATGACAGAG	2266
OY	4631	ATCTGCCCCGCGCACTTGCCCAATAGACGCAATCCTTCCGCTTCAGTGACATGCTC	4690
Db	2265	ATCTGCCCCGCGCACTTGCCCAATAGACGCAATCCTTCCGCTTCAGTGACATGCTC	2206
OY	4691	GAGACAGCTGCGGAAGGAGACGCCGCTGTGGCAGACAGATAGCGCGCTGCTCGTC	4750
Db	2205	GAGACAGCTGCGGAAGGAGACGCCGCTGTGGCAGACAGATAGCGCGCTGCTCGTC	2146
OY	4751	CTGCAATTCATTACGGGCAACCGACAGGTCCGTCTTGACAAAAAGAAACCGGCGCCCTGT	4810
Db	2145	TTTGCAATTCATTACGGGCAACCGACAGGTCCGTCTTGACAAAAAGAAACCGGCGCCCTGT	2086
OY	4811	CGCTGACAGCCGGAACACAGCGGATCATAGACAGCCGATTTGTCTGTTGTCCACATCAT	4870
Db	2085	CGCTGACAGCCGGAACACAGCGGATCATAGACAGCCGATTTGTCTGTTGTCCACATCAT	2026
OY	4871	GCCGATATGCTCTTCCACCCCAAGGCGCGGAGAACTTGCGTGAATCATTTTTCAT	4930
Db	2025	GCCGATATGCTCTTCCACCCCAAGGCGCGGAGAACTTGCGTGAATCATTTTTCAT	1966
OY	4931	CATCGAAGACATCTCATCTGTCTCTTGAATCAGATCTTGATCCCTGCGCCATCAGAT	4990
Db	1965	CATCGAAGACATCTCATCTGTCTCTTGAATCAGATCTTGATCCCTGCGCCATCAGAT	1906
OY	4991	CTTTGGCGGCAAGAACCATCATGATTAATTTTTCAGGCTTCCCAACTTACAGAGG	5050



Db 1905 CCTTGGCGGCGAAGAAAGCCATCCAGTTTACTTTGACAGGGCTTCCAACTTACAGAGGG 1846  
Qy 5051 GCGCCAGCTGGCAATTCGGTTCCGTTGCTGTCCATAAACCAGCCAGTACGATCG 5110  
Db 1845 GCGCCAGCTGGCAATTCGGTTCCGTTGCTGTCCATAAACCAGCCAGTACGATCG 1786  
Qy 5111 CCATGTAAAGCCCACTGCAAGCTACCTGCTTTCTTTGGCTTGGCTTTCCCTTGTCCA 5170  
Db 1785 CCATGTAAAGCCCACTGCAAGCTACCTGCTTTCTTTGGCTTGGCTTTCCCTTGTCCA 1726  
Qy 5171 GATAGCCCAAGTACGATTCATCCGGGGTCAGACCGTTTCCGAGCTGGCTTTCTTA 5230  
Db 1725 GATAGCCCAAGTACGATTCATCCGGGGTCAGACCGTTTCCGAGCTGGCTTTCTTA 1666  
Qy 5231 CGTG 5234  
Db 1665 CGTG 1662

RESULT 4  
US-11-193-750-10/c  
; Sequence 10, Application US/11193750  
; Publication No US20050273873A1  
; GENERAL INFORMATION:  
; APPLICANT: Avigenics, Inc  
; TITLE OF INVENTION: MODIFICATION OF THE GENOME BY INTRODUCTION OF LARGE NUCLEIC ACID  
; FILE REFERENCE: AVI-025CIP4  
; CURRENT APPLICATION NUMBER: US/11/193,750  
; CURRENT FILING DATE: 2005-07-29  
; PRIOR APPLICATION NUMBER: US/11/068,155  
; PRIOR FILING DATE: 2005-02-28  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 10  
; LENGTH: 6233  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Plasmid PCR-XL-TOPO-CMV-pur-atcb  
US-11-193-750-10

Query Match 30.9%; Score 1634.4; DB 17; Length 6233;  
Best Local Similarity 80.6%; Pred. No. 0;  
Matches 2082; Conservative 0; Mismatches 211; Indels 291; Gaps 3;

Qy 2942 CTTCCGCTTCTCGCTCACTACCTGCTGCGCTGCTGCTGCTGCTGCGAGCGGTAT 3001  
Db 6233 CTTCCGCTTCTCGCTCACTACCTGCTGCGCTGCTGCTGCTGCTGCGAGCGGTAT 6174  
Qy 3002 CAGCTCACTCAAAAGCGGTATACGTTATCCAGAGATCAGGGATTAAGCAGAGAAAG 3061  
Db 6173 CAGCTCACTCAAAAGCGGTATACGTTATCCAGAGATCAGGGATTAAGCAGAGAAAG 6114  
Qy 3062 ACATGTAGCAAAAGGCGCAGCAAAAGGCGAGAAACCTTAATAAAGCGCGCTTGTGCGCT 3121  
Db 6113 ACATGTAGCAAAAGGCGCAGCAAAAGGCGAGAAACCTTAATAAAGCGCGCTTGTGCGCT 6054  
Qy 3122 TTTTTCATAGGCTCCGCCCCCTGTAAGCATCAAAATTCAGCGCTCAAGTCAAGGT 3181  
Db 6053 TTTTTCATAGGCTCCGCCCCCTGTAAGCATCAAAATTCAGCGCTCAAGTCAAGGT 5994  
Qy 3182 GGGCAAAACCGACAGATTAAGATACAGAGGGTTTCCCGTGAAGCTCCCTGTCG 3241  
Db 5993 GGGCAAAACCGACAGATTAAGATACAGAGGGTTTCCCGTGAAGCTCCCTGTCG 5994  
Qy 3242 GCTCTCTGTTCCAGACCTGCGCTTACCGGATACCTGCGCTTTCTCCCTTGGGAA 3301  
Db 5933 GCTCTCTGTTCCAGACCTGCGCTTACCGGATACCTGCGCTTTCTCCCTTGGGAA 5874  
Qy 3302 GCGTGGCGCTTTCTCATAGCTCAGCGTGTAGTATCTCAGTTGGTGGTGGTCT 3361  
Db 5873 GCGTGGCGCTTTCTCATAGCTCAGCGTGTAGTATCTCAGTTGGTGGTGGTCT 5814

Qy 3362 CCAAGCTGGGCTGTGTGACGAAACCCCGTTACAGCCCGACGCTGCGCTTATCCGGTA 3421  
Db 5813 CCAAGCTGGGCTGTGTGACGAAACCCCGTTACAGCCCGACGCTGCGCTTATCCGGTA 5754  
Qy 3422 ACTATCGTCTTGAAGTCCAAACCGGTAAAGACAGATTAATGCGACTGACAGCAGCTG 3481  
Db 5753 ACTATCGTCTTGAAGTCCAAACCGGTAAAGACAGATTAATGCGACTGACAGCAGCTG 5694  
Qy 3482 GTAACAGATTAAGCAGAGCCAGATTAATGAGCGGTGCTACAGAGTTCTTGAAGTGGC 3541  
Db 5693 GTAACAGATTAAGCAGAGCCAGATTAATGAGCGGTGCTACAGAGTTCTTGAAGTGGC 5634  
Qy 3542 CTAATACGGCTACACTGAGAAAGATTAATGAGTGTGCTGCTGCTGAGAGCAGTTA 3601  
Db 5633 CTAATACGGCTACACTGAGAAAGATTAATGAGTGTGCTGCTGCTGAGAGCAGTTA 5574  
Qy 3602 CTTTCGAAAAAGATTGATAGCTCTTGATCCGCAACCAACACCGCTGTAGCGGTG 3661  
Db 5573 CTTTCGAAAAAGATTGATAGCTCTTGATCCGCAACCAACACCGCTGTAGCGGTG 5514  
Qy 3662 GTTTTGTGTTTTCAGACAGCAGATTACGCGCAGAAAAAGATCTCAAGAGATCTT 3721  
Db 5513 GTTTTGTGTTTTCAGACAGCAGATTACGCGCAGAAAAAGATCTCAAGAGATCTT 5454  
Qy 3722 TGATCTTTTTCAGAGGGGTGAGGCTCAGTGAAGAAAGAAATCTCAGTTAAGGATTTTG 3781  
Db 5453 TGATCTTTTTCAGAGGGGTGAGGCTCAGTGAAGAAAGAAATCTCAGTTAAGGATTTTG 5394  
Qy 3782 TCATGAGATTATC----- 3794  
Db 5393 TCATGAGATTATCAAAAAAGATCTTCACTAGATCTTTAATTAATAAGATTTTA 5334  
Qy 3795 -----GTGACCA 3802  
Db 5333 GCACGTGCAAGTCTGCTCTCGGCAAGATGACAGCAAGTTCCGCGCGCGCGCA 5274  
Qy 3803 AAGCGGCATCGTGCCTCCCACTCGCAGATTGGGGGACATGATGGCGGATAGCGCG 3862  
Db 5273 GAGCGAATCTCCGCGCCCAAGGCTGCTCGCGATCTGATGATGCGCGCGCGAGGCT 5214  
Qy 3863 TGCTGTTTCTGTGATCCGACGAGATTGCACTGCGCGGTGAATCTCCGCGAGTCTTCA 3922  
Db 5213 CCGGGAAGTTGTGGAACACGACCTCGACCACTCGGGGTACAGTCTGTCAGGCGCGCA 5154  
Qy 3923 GCG----- 3925  
Db 5153 CCGCAACCCAGCGCGGTGTGTCGCGACCACTGTGCTCTGGAACCGCGCTGATGAACA 5094  
Qy 3926 ---TCAGGACAGAGTGAACCACTCGCGAGGGATGAGACCCGGGTGGCGGAAGACT 3982  
Db 5093 GGGTCAAGTGTCCCGGACCAACCGGCGAAGTGTCTCCAGCAATCCCGGAGAAC 5034  
Qy 3983 CAGCATGAGATCCCGCGCTGAGGATCATCCAGCGCGGCTCCGGAATAAGATTCCGA 4042  
Db 5033 CAGCGCGGTGTGGAATTCAGACCGCTCCCGGACAGTGGCGCGGTGAGCACCGGA 4974  
Qy 4043 AGCCCAACTTTTATAGAGCGCGGTGAATTCGAATCTCGTATGAGGAGTTGGCG 4102  
Db 4973 CCGCACTGTCAACTTGGCCATGTGTGCTCTCAAGTCTATTTAAGCAATTTATC 4914  
Qy 4103 TCGCTGTGTGCTATTTGCAACCCAGAGTCCG----- 4137  
Db 4913 AGGGTATTTGTCTCATAGAGCGGATTAATTTAATTTAAGAAAAATAACAAATAG 4854  
Qy 4138 ----- 4137  
Db 4853 GGGTTCGCGCACATTTCCCGAAAGTGCACCTGTATGCGGTGTAATATCCGACAG 4794  
Qy 4138 -----CTCAGAAAGATC 4150  
Db 4793 ATGCGTAAGAGAAAAATACCGCATCAGAAATTTGTAAGCGTTAATTAATTCAGAAAGATC 4734





QY 3366 GCTGGGCTGTGTGACGAAACCCCGCTTCAAGCCGACGCTGCGCTTATCCGGTAACCTA 3425  
 DB 2072 GCTGGGCTGTGTGACGAAACCCCGCTTCAAGCCGACGCTGCGCTTATCCGGTAACCTA 2131  
 QY 3426 TCGTCTTGAATGCTCAACCCGGTAAGACACGACTTATCCGCACTGGACAGCACTGGTAA 3485  
 DB 2132 TCGTCTTGAATGCTCAACCCGGTAAGACACGACTTATCCGCACTGGACAGCACTGGTAA 2191  
 QY 3486 CAGGATTAGCAGAGCGAGGTATGTAAGCGGCTACAGAGTCTTGAAGTGGTGGCCCTAA 3545  
 DB 2192 CAGGATTAGCAGAGCGAGGTATGTAAGCGGCTACAGAGTCTTGAAGTGGTGGCCCTAA 2251  
 QY 3546 CTACGGCTACACTAGAAAGACATATTTGATCTGCGCTCTGCTGAAGCCAGTAACTT 3605  
 DB 2252 CTACGGCTACACTAGAAAGACATATTTGATCTGCGCTCTGCTGAAGCCAGTAACTT 2311  
 QY 3606 CGGAAAAAGAGTTGGTGTGCTTTGATCCGGCAAAACCAACCGCTGGTACGGTGGTT 3665  
 DB 2312 CGGAAAAAGAGTTGGTGTGCTTTGATCCGGCAAAACCAACCGCTGGTACGGTGGTT 2371  
 QY 3666 TTTTGTTCGAAGCAGAGATTACGCGCAAAAAAAGATCTGAAGAGATCCCTTGAT 3725  
 DB 2372 TTTTGTTCGAAGCAGAGATTACGCGCAAAAAAAGATCTGAAGAGATCCCTTGAT 2431  
 QY 3726 CTTTCTTACCGGGGTCTGACGCTCAGTGGAAAGAAACTCAGCTTAAGGATTTTGTCTAT 3785  
 DB 2432 CTTTCTTACCGGGGTCTGACGCTCAGTGGAAAGAAACTCAGCTTAAGGATTTTGTCTAT 2449  
 QY 3786 GAGATTATCGTCAACAAAGCGGCAATCGTCCCTCCCACTCTGCAAGTTCCGGGGCATG 3845  
 DB 2450 GAGATTATCGTCAACAAAGCGGCAATCGTCCCTCCCACTCTGCAAGTTCCGGGGCATG 2449  
 QY 3846 GATGCGGGAATAGCGCGTGTGTTTCTGTGATGCCAGCGATTGTGCACTGCCGGTAGAA 3905  
 DB 2450 GATGCGGGAATAGCGCGTGTGTTTCTGTGATGCCAGCGATTGTGCACTGCCGGTAGAA 2449  
 QY 3906 CTCGCGAGGTGCTGCTCAGCCTCAGGCAAGCTGAACTCGGAGGGATCGAGGCC 3965  
 DB 2450 CTCGCGAGGTGCTGCTCAGCCTCAGGCAAGCTGAACTCGGAGGGATCGAGGCC 2449  
 QY 3966 GGGGTGGCGAAGATCTCAGCATGAGATCCCGCGCTGAGAGATCTCAGCGGCGTC 4025  
 DB 2450 GGGGTGGCGAAGATCTCAGCATGAGATCCCGCGCTGAGAGATCTCAGCGGCGTC 2449  
 QY 4026 CCGGAAAAAGATCCGGAAGCCCACTTTCATAGAGCGCGGTGGAATCGAATCTCG 4085  
 DB 2450 CCGGAAAAAGATCCGGAAGCCCACTTTCATAGAGCGCGGTGGAATCGAATCTCG 2449  
 QY 4086 TGATGCGAGGTGGCGTCTGCTGTGCTGATTTGCAACCCAGAGTCCCGCTCAGAG 4145  
 DB 2450 TGATGCGAGGTGGCGTCTGCTGTGCTGATTTGCAACCCAGAGTCCCGCTCAGAG 2459  
 QY 4146 AACTCGTCAAGAAAGCGATGAAAGCGATGCTGCGAATCGGAGCGCGATACCGTAA 4205  
 DB 2460 AACTCGTCAAGAAAGCGATGAAAGCGATGCTGCGAATCGGAGCGCGATACCGTAA 2519  
 QY 4206 AGCAGAGAGAGGGGTAGCGCAATTCGCGCGCAAGCTTTCAGCAATATCACGGTAGCC 4265  
 DB 2520 AGCAGAGAGAGGGGTAGCGCAATTCGCGCGCAAGCTTTCAGCAATATCACGGTAGCC 2579  
 QY 4266 AAGCGTATGCTGATAGCGGTCCGACACCCAGCGGCGCAAGTGCATGATTCAGAA 4325  
 DB 2580 AAGCGTATGCTGATAGCGGTCCGACACCCAGCGGCGCAAGTGCATGATTCAGAA 2639  
 QY 4326 AAGCGGCAATTTTCCACATGATATTCGCAAGAGGCGCATCGCCATGGTTCACAGAGA 4385  
 DB 2640 AAGCGGCAATTTTCCACATGATATTCGCAAGAGGCGCATCGCCATGGTTCACAGAGA 2699  
 QY 4386 TCGTGGCGGTGCGGCGATGGCGCTTGAAGCTGGCGAAACGTTTCGGTGGCGAGAGCCC 4445  
 DB 2700 TCGTGGCGGTGCGGCGATGGCGCTTGAAGCTGGCGAAACGTTTCGGTGGCGAGAGCCC 2759  
 QY 4446 TGATGCTCTTCTGCTCAGATCATCTGATCGAACAAAGCCGGCTTCATCCAGTACGTGCT 4505

DB 2760 TGATGCTCTTCTGCTCAGATCATCTGATTCGAAACGCGCTTCATCCGATACGTGCT 2819  
 QY 4506 CGCTGCATGCGATGTTTCCGCTTGTGGTCCGATGGGCGAGTACCGGATCAAGCGTATGC 4565  
 DB 2820 CGCTGCATGCGATGTTTCCGCTTGTGGTCCGATGGGCGAGTACCGGATCAAGCGTATGC 2879  
 QY 4566 AGCGCGCGAATGATGATGAGCGCATGATGATCTTTCGCGAGAGAGCAAGGTGATGATAC 4625  
 DB 2880 AGCGCGCGAATGATGATGAGCGCATGATGATCTTTCGCGAGAGAGCAAGGTGATGATAC 2939  
 QY 4626 AGGAGATCTGCCCCCGCACTTCGCCAATAGACAGCCAGTCCCTCCGCTTCAAGTACA 4685  
 DB 2940 AGGAGATCTGCCCCCGCACTTCGCCAATAGACAGCCAGTCCCTCCGCTTCAAGTACA 2999  
 QY 4686 AGCTGAGCACAGCTGGCGAAGAACCCCGTGTGCGCAGCCAGATAGCCGCGTGC 4745  
 DB 3000 AGCTGAGCACAGCTGGCGAAGAACCCCGTGTGCGCAGCCAGATAGCCGCGTGC 3059  
 QY 4746 TCGTCTGCAAGTTCATTCAGGGGCAAGGAGAGTCCGCTTGAAGAAAGAACGGGGCGC 4805  
 DB 3060 TCGTCTGCAAGTTCATTCAGGGGCAAGGAGAGTCCGCTTGAAGAAAGAACGGGGCGC 3119  
 QY 4806 CCTGCGCTGACAGCCGGAACAAGCGGCGATCAGAGAGCCGATGCTGTTGTGCCAG 4865  
 DB 3120 CCTGCGCTGACAGCCGGAACAAGCGGCGATCAGAGAGCCGATGCTGTTGTGCCAG 3179  
 QY 4866 TCATAGCGCAATAGCTTCTCCACCCAGAGCGGCGGAGAACCTGCGTCAATCTTGT 4925  
 DB 3180 TCATAGCGCAATAGCTTCTCCACCCAGAGCGGCGGAGAACCTGCGTCAATCTTGT 3239  
 QY 4926 TCATAGCGCAATAGCTTCTCCACCCAGAGCGGCGGAGAACCTGCGTCAATCTTGT 4985  
 DB 3240 TCATAGCGCAATAGCTTCTCCACCCAGAGCGGCGGAGAACCTGCGTCAATCTTGT 3299  
 QY 4986 CAGATCCTTGGCGCAAGAAAGCATCAGTTACTTTCAGAGGCTTCCCACTTACCA 5045  
 DB 3300 CAGATCCTTGGCGCAAGAAAGCATCAGTTACTTTCAGAGGCTTCCCACTTACCA 3359  
 QY 5046 GAGGCGCGCCCAAGTGGCAATTCGAGTTCGCTGCTGCTGCTCAATAAACCGCCAGTAC 5105  
 DB 3360 GAGGCGCGCCCAAGTGGCAATTCGAGTTCGCTGCTGCTGCTCAATAAACCGCCAGTAC 3419  
 QY 5106 TATCGCATGTAGCCCATGCAAGCTACCTGCTTCTT 5146  
 DB 3420 TATCGCATGTAGCCCATGCAAGCTACCTGCTTCTT 3460

RESULT 6  
 US-10-764-818A-12  
 ; Sequence 12, Application US/10764818A  
 ; Publication No. US20040204358A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ADVISYS  
 ; TITLE OR INVENTION: GROWTH HORMONE RELEASING HORMONE ("GHRH") TREATMENT DECREASES CULI  
 ; FILE REFERENCE: 108328.00170 - AVSI-0033  
 ; CURRENT APPLICATION NUMBER: US/10764,818A  
 ; NUMBER OF SEQ ID NOS: 30  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 12  
 ; LENGTH: 3534  
 ; TYPE: DNA  
 ; ORGANISM: artificial sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Sequence for the TI-GHRH plasmid.  
 US-10-764-818A-12

Query Match 30.4%; Score 1603.8; DB 11; Length 3534;  
 Best Local Similarity 82.8%; Pred. No. 0;  
 Matches 2022; Conservative 0; Mismatches 27; Indels 392; Gaps 1;

QY	2706	CTAAGCGTAATCATAGGTATATAGCTGTTTCCGTGTGTAATTGTTATCCGCTCACAATATCC	2765
Db	1412	CTTGCGTAATCATAGGTATATAGCTGTTTCCGTGTGTAATTGTTATCCGCTCACAATATCC	1471
QY	2766	ACAACAATACAGAGCCGGAACATATAATGTAAAGCTCGGGGTGGCTTAATAGTAGACTA	2825
Db	1472	ACAACAATACAGAGCCGGAACATATAATGTAAAGCTCGGGGTGGCTTAATAGTAGACTA	1531
QY	2826	ACTCAATTAATTTGCGTTGCGCTCACTGCCCCGCTTTCAGTCGGGAAACTGTCTGTCCA	2885
Db	1532	ACTCAATTAATTTGCGTTGCGCTCACTGCCCCGCTTTCAGTCGGGAAACTGTGTGTCCA	1591
QY	2886	GCTGCATTAATGAATCCGCGCAACGCGGGGAGAGGCGGTTTGGGTATTTGGGCGCTCTC	2945
Db	1592	GCTGCATTAATGAATCCGCGCAACGCGGGGAGAGGCGGTTTGGGTATTTGGGCGCTCTTC	1651
QY	2946	CGCTTCTCGCTCACTGACTGCTGCGTGGTGGTTCGGCTCGGCGAGCGGATATCAGC	3005
Db	1652	CGCTTCTCGCTCACTGACTGCTGCGTGGTGGTTCGGCTCGGCGGAGCGGATATCAGC	1711
QY	3006	TCACCTCAAAAGCGGGTAATACGGTTATCCACAGATACAGGGGATPAACGCAAGAAAGAACT	3065
Db	1712	TCACCTCAAAAGCGGGTAATACGGTTATCCACAGAAATCAGGGGATPAACGAGAAAGAACT	1771
QY	3066	GTGAGCAAAAGCGCAGCAAAAAGCGCAGGAAACCGTAAAAAAGGCCGCGTGTGCTGCGGTTTT	3125
Db	1772	GTGAGCAAAAGCGCAGCAAAAAGCGCAGGAAACCGTAAAAAAGGCCGCGTGTGCGGTTTT	1831
QY	3126	CCATATAGCTCCGCCCCCTCTGACAGAGCATCAAAAATATGACGTCMAAGTCAGAGGTGGC	3185
Db	1832	CCATATAGCTCCGCCCCCTCTGACAGAGCATCAAAAATATGAGGTCMAAGTCAGAGGTGGC	1891
QY	3186	AAACCCGACAGAGACTATTAAGATACAGAGCGTTTCCCTCGTGAAGCTCCCTCGGCGCTC	3245
Db	1892	AAACCCGACAGAGACTATTAAGATACAGAGCGTTTCCCTCGTGAAGCTCCCTCGGCGCTC	1951
QY	3246	TTCCTGTTCCGACCCCTGCGCTTACCGGATACCTGTCCGCTTTCTCCCTTGGGAAACGT	3305
Db	1952	TTCCTGTTCCGACCCCTGCGCTTACCGGATACCTGTCCGCTTTCTCCCTTGGGAAACGT	2011
QY	3306	GGCGCTTTCATATAGCTCAAGCTGTAGAGTATCTCAGTTCGGTGAAGTCCGTGCGTCCAA	3365
Db	2012	GGCGCTTTCATATAGCTCAAGCTGTAGAGTATCTCAGTTCGGTGAAGTCCGTGCGTCCAA	2071
QY	3366	GCTGGGCTGTGTGACGAACCCCGCTTTCAGGCCGACCGCTGCGCTTATCCGGTAACTA	3425
Db	2072	GCTGGGCTGTGTGACGAACCCCGCTTTCAGGCCGACCGCTGCGCTTATCCGGTAACTA	2131
QY	3426	TTCGCTTAGGTCCAACCCCGGTAAACAGAGCTTATCCCACTGGCAGCAGCCTAGTTAA	3485
Db	2132	TTCGCTTAGGTCCAACCCCGGTAAACAGAGCTTATCCCACTGGCAGCAGCCTAGTTAA	2191
QY	3486	CAGGATTTAGCAGAGCGAGTATGTAGGCGGTCTACAGAGTTCCTTGAAGTGTGGCTTAA	3545
Db	2192	CAGGATTTAGCAGAGCGAGTATGTAGGCGGTCTACAGAGTTCCTTGAAGTGTGGCTTAA	2251
QY	3546	CTACGGCTTACCTATGAAGAAACAGTATTTGGTATTTGCGCTCTGTGAAGCAAGTTACCTT	3605
Db	2252	CTACGGCTTACCTATGAAGAAACAGTATTTGGTATTTGCGCTCTGTGAAGCAAGTTACCTT	2311
QY	3606	CGGAAAAAGAGTTGGTAGCTCTTGAATCCGGCAAAACAACACCGCTGTAGCGGTGTTT	3665
Db	2312	CGGAAAAAGAGTTGGTAGCTCTTGAATCCGGCAAAACAACACCGCTGTAGCGGTGTTT	2371
QY	3666	TTTTGTTTGCAGAGCAGATTTACGCGCAGAAAAAAGATCTTCAAGAAATCCTTTGAT	3725
Db	2372	TTTTGTTTGCAGAGCAGATTTACGCGCAGAAAAAAGATCTTCAAGAAATCCTTTGAT	2431
QY	3726	CTTTTTCACGGGGCTGACCGCTCAGTGTGAAGGAACTCAAGTTTGGTCAAT	3785
Db	2432	CTTTTTCACGGGGCTGACCGCTCAGTGTGAAGGAACTCAAGTTTGGTCAAT	2449
QY	3786	GAGATTAATCGTCAACAAAGCGCAACGTGTCCTCCCACTCTGCAAGTTGGGGGAGT	3845

Db	2450	-----	2449
QY	3846	GATGCGGATATAGCCGCTGCTGTTTCTGTATGCGGATTTTGCACTGCGGTAGAA	3905
Db	2450	-----	2449
QY	3906	CTCCGCGAGGTGCTGTCACACTCAGGACACACTGAACCACTCCGCGAGGGATGAGCC	3965
Db	2450	-----	2449
QY	3966	GGGGTGGCGAAGAACTCCAGATGATCCCGCGTGGAGATCATCAGCCGCGTC	4025
Db	2450	-----	2449
QY	4026	CCGGAATTCGATCCGAAGCCCAACTTTATAGAGGCGGTGAATCGAATCTCG	4085
Db	2450	-----	2449
QY	4086	TGATGCGAGTTGGGCGTCCGTTGGTCCGATTTCCAACTCCGATCAGAGTCCCGCTCAGAG	4145
Db	2450	-----	2449
QY	4146	AACTGTCAGAAAGCGCATAGAAAGCGATGCGCTGCGAATCGGAGCGGCGATACCGTAA	4205
Db	2460	AACTGTCAGAAAGCGCATAGAAAGCGATGCGCTGCGAATGCGAGCGGCGATACCGTAA	2519
QY	4206	AGCAGAGAAAGCGGTGACGCCATTTCCGCGCAAGCTCTTCAGCAATATCACGGGTAGCC	4265
Db	2520	AGCAGAGAAAGCGGTGACGCCATTTCCGCGCAAGCTCTTCAGCAATATCACGGGTAGCC	2579
QY	4266	AAAGCTATGCTGATAGCGGTCCGCGCAACCCAGCCGCGCAGTGAATTCAGAA	4325
Db	2580	AAAGCTATGCTGATAGCGGTCCGCGCAACCCAGCCGCGCAGTGAATTCAGAA	2639
QY	4326	AAAGCGCCATTTTCACCATGATATTCGGCAAGCAGGCATCGCCATGGTCAACGACAGA	4385
Db	2640	AAAGCGCCATTTTCACCATGATATTCGGCAAGCAGGCATCGCCATGGTCAACGACAGA	2699
QY	4386	TCCTGCGCGTGGGCAATGCGCGCTTGAGCTTGCGCAAGATTGGCTGGCGAGCCCC	4445
Db	2700	TCCTGCGCGTGGGCAATGCGCGCTTGAGCTTGCGCAAGATTGGCTGGCGAGCCCC	2759
QY	4446	TGATGCTCTTGTCAGATCATCTGATTCGACAAACCGGCTTCATCCGATACGTC	4505
Db	2760	TGATGCTCTTGTCAGATCATCTGATTCGACAAACCGGCTTCATCCGATACGTC	2819
QY	4506	CGCTCGATGCGATGTTTCGTTGGTGGTTCGATGGCAGGTAGCCGATCAAGCGTATGC	4565
Db	2820	CGCTCGATGCGATGTTTCGTTGGTGGTTCGATGGCAGGTAGCCGATCAAGCGTATGC	2879
QY	4566	AGCCGCGCATTTGATCAGCCATGATGATATCTTTCTCGCGAGGACGAGGTGATGAC	4625
Db	2880	AGCCGCGCATTTGATCAGCCATGATGATATCTTTCTCGCGAGGACGAGGTGATGAC	2939
QY	4626	AGGAGATTCGAGCCCGGCACTTGCGCCCAATAGACGCAATGCCCTTCCGCTTCAATGACA	4685
Db	2940	AGGAGATTCGAGCCCGGCACTTGCGCCCAATAGACGCAATGCCCTTCCGCTTCAATGACA	2999
QY	4686	ACGTCGAGCAGCTGCGCAAGAACGCGCGTGGCCACGACGATAGCCGCGCTGCC	4745
Db	3000	ACGTCGAGCAGCTGCGCAAGAACGCGCGTGGCCACGACGATAGCCGCGCTGCC	3059
QY	4746	TCGTCCTGCAATTCATTCAGGGCAACCGGACAGGTCCGTTCTTGAACAAAAGAACCGGCGC	4805
Db	3060	TCGTCCTGCAATTCATTCAGGGCAACCGGACAGGTCCGTTCTTGAACAAAAGAACCGGCGC	3119
QY	4806	CCCTGCGCTACAGCCGGAACACGCGCGCATCAGAGAGCGGATGCTGTCGTCAG	4865
Db	3120	CCCTGCGCTACAGCCGGAACACGCGCGCATCAGAGAGCGGATGCTGTCGTCAG	3179
QY	4866	TCATAGCGGATATGCTCTCCACCAAGCGCGCGAGAACCTTCGTCATTCATCTTGT	4925

Db 3180 TCATAGCCGAATAGCCTCTCCACCCAGCGCGGAGAACTGCGTGAATCATCTTGT 3239  
Qy 4926 TCATCATGCGCAAGCATCTCATCTGTCTTGTATGAGATCTTGATCCCTGCGCAT 4985  
Db 3240 TCATCATGCGCAAGCATCTCATCTGTCTTGTATGAGATCTTGATCCCTGCGCAT 3299  
Qy 4986 CAGATCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGAGAGGCTTCCCACTTACCA 5045  
Db 3300 CAGATCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGAGAGGCTTCCCACTTACCA 3359  
Qy 5046 GAGGCGCGCCCAAGCTGGCAATTCGGTTCCTGCTGTCTGCAATAAAACCGCCAGTCTAGC 5105  
Db 3360 GAGGCGCGCCCAAGCTGGCAATTCGGTTCCTGCTGTCTGCAATAAAACCGCCAGTCTAGC 3419  
Qy 5106 TATGCGCATGTAGCCCACTGCAAGCTACCTCTTCTCTT 5146  
Db 3420 AACTGTTGGAAAGGCGCATCGGTGCGGCGCTCTTCCGTAAT 3460

RESULT 7  
US-10-764-818A-13  
; Sequence 13, Application US/10764818A  
; Publication No. US20040204358A1  
; GENERAL INFORMATION:  
; APPLICANT: ADVANIS  
; TITLE OF INVENTION: GROWTH HORMONE RELEASING HORMONE ("GHRH") TREATMENT DECREASES CUI  
; FILE REFERENCE: 108328.00170 - AVSI-0033  
; CURRENT APPLICATION NUMBER: US/10764, 818A  
; CURRENT FILING DATE: 2004-01-26  
; SOFTWARE: Patent version 3.1  
; SEQ ID NO 13  
; LENGTH: 3534  
; TYPE: DNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Nucleic acid sequence for the TV-GHRH plasmid.  
US-10-764-818A-13

Query Match 30.4%; Score 1603.8; DB 11; Length 3534;  
Best Local Similarity 82.8%; Pred. No. 0;  
Matches 202; Conservative 0; Mismatches 27; Indels 392; Gaps 1;

Qy 2706 CTAGACGTAATCAAGTCATGCTGCTGTTCTCTGTGTAATGTTATCCGCTCACAATTC 2765  
Db 1412 CTGGCGTAATCATGTCATAGCTGTTCTGTGTAATGTTATCCGCTCACAATTC 1471  
Qy 2766 ACAACAATAGAGCCGGAAGCATAAAGTGAAGCTGGGGTCTTAATAGTAGCTA 2825  
Db 1472 ACAACAATAGAGCCGGAAGCATAAAGTGAAGCTGGGGTCTTAATAGTAGCTA 1531  
Qy 2826 ACTCACATTAATGCGTTCGCTCACTGCGCTTTTCCAGTCGGGAAACCTGTCTGCCA 2885  
Db 1532 ACTCACATTAATGCGTTCGCTCACTGCGCTTTTCCAGTCGGGAAACCTGTCTGCCA 1591  
Qy 2886 GCTGCAATTAATGATCGGCGCAAGCGCGGGAGAGGCGGTTTGGCTATTTGGCGCTTTC 2945  
Db 1592 GCTGCAATTAATGATCGGCGCAAGCGCGGGAGAGGCGGTTTGGCTATTTGGCGCTTTC 1651  
Qy 2946 CGCTTCTCGCTCACTGCTGCTGCGCTCGTTCGCTGCGGCGAGGCGATACG 3005  
Db 1652 CGCTTCTCGCTCACTGCTGCTGCGCTCGTTCGCTGCGGCGAGGCGATACG 1711  
Qy 3006 TCACCTCAAGCGGTAATACGCTTATCCAGAAATCAGGGGATTAACGAGAAAGAAAT 3065  
Db 1712 TCACCTCAAGCGGTAATACGCTTATCCAGAAATCAGGGGATTAACGAGAAAGAAAT 1771  
Qy 3066 GTGAGCAAAAGGCGAGCAAGAAAGCGCAAGAACCTTAAGAAAGCGCTTCTGGGTTTTT 3125  
Db 1772 GTGAGCAAAAGGCGAGCAAGAAAGCGCAAGAACCTTAAGAAAGCGCTTCTGGGTTTTT 1831  
Qy 3126 CCAATAGGCTCGCCCGCTCGAGCATCAAAAAATCGACGCTCAAGTCAGAGTGGCG 3185

Db 1832 CCATAGGCTCGCCCGCTGACAGACATCAAAAAATGAGGCTCAATCAGAGGTGCG 1891  
Qy 3186 AAACCCGACAGACTATTAAGATACAGAGGCTTTCCCTGAAAGCTCCTGTGCGTTC 3245  
Db 1892 AAACCCGACAGACTATTAAGATACAGAGGCTTTCCCTGAAAGCTCCTGTGCGTTC 1951  
Qy 3246 TCGTGTCCGACCGTGGCGCTTAACGGAATACCTGTCCGCTTTCTCCCTTGGGAAAGGT 3305  
Db 1952 TCGTGTCCGACCGTGGCGCTTAACGGAATACCTGTCCGCTTTCTCCCTTGGGAAAGGT 2011  
Qy 3306 GCGCGCTTCTCATAGCTCACGCTGTAGGTATCTGAGTTCGCTGTAAGTCTGTTGCTCCAA 3365  
Db 2012 GCGCGCTTCTCATAGCTCACGCTGTAGGTATCTGAGTTCGCTGTAAGTCTGTTGCTCCAA 2071  
Qy 3366 GCTGGGCTGTGTGACAGAACCCCGCTTACGCGGACCGCTGCGCTTATCCGTAACCTA 3425  
Db 2072 GCTGGGCTGTGTGACAGAACCCCGCTTACGCGGACCGCTGCGCTTATCCGTAACCTA 2131  
Qy 3426 TCGTGTCCGACCGTGGCGCTTAACGGAATACCTGTCCGCTTTCTCCCTTGGGAAAGGT 3485  
Db 2132 TCGTGTCCGACCGTGGCGCTTAACGGAATACCTGTCCGCTTTCTCCCTTGGGAAAGGT 2191  
Qy 3486 CAGGATTAGCAGACGAGATGTAGCGGCTGCTACAGAGTTCTTGAAGTGTGGCTTAA 3545  
Db 2192 CAGGATTAGCAGACGAGATGTAGCGGCTGCTACAGAGTTCTTGAAGTGTGGCTTAA 2251  
Qy 3546 CTACGCTACACTAGAAAGAAAGATTTGATGCTGCTGCTGTGAAGCAGTTACCTT 3605  
Db 2252 CTACGCTACACTAGAAAGAAAGATTTGATGCTGCTGCTGTGAAGCAGTTACCTT 2311  
Qy 3606 CGGAAAAAGGTGTGCTGCTTGAATCCGCAACCAACCGCTGTAGCGGTGTT 3665  
Db 2312 CGGAAAAAGGTGTGCTGCTTGAATCCGCAACCAACCGCTGTAGCGGTGTT 2371  
Qy 3666 TTTTGTTCGACAGAGATTAAGCGCGCAAGAAAGATCTCAAGAAAGTCTTTGAT 3725  
Db 2372 TTTTGTTCGACAGAGATTAAGCGCGCAAGAAAGATCTCAAGAAAGTCTTTGAT 2411  
Qy 3726 CTTTTCACGCGGCTGTAGCGCTCAGTGAAAGAAACTCAGTTAAGGATTTTGTCTAT 3785  
Db 2432 CTTTTCACGCGGCTGTAGCGCTCAGTGAAAGAAACTCAGTTAAGGATTTTGTCTAT 2449  
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Db 2449 GAGATTATCGTCACAAAGCGCATGTCCTCCCACTCTGCAAGTTCGGGGCATG 2499  
Qy 3846 GATGCGGATAGCCGCTGCTGCTTCTGATGTCGACGGAATTTGCACTGCGGTAGAA 3905  
Db 2499 GATGCGGATAGCCGCTGCTGCTTCTGATGTCGACGGAATTTGCACTGCGGTAGAA 2549  
Qy 3906 CTCGCGAGTCTGACGCTCAGGACGAGCTGAACCACTGCGAGGGAGTAGAGCCC 3965  
Db 2549 CTCGCGAGTCTGACGCTCAGGACGAGCTGAACCACTGCGAGGGAGTAGAGCCC 2605  
Qy 3966 GGGGTGGGCAAGAACTCCAGCATGAGATCCCGCGCTGAGAGATCATCAGCGGCTC 4025  
Db 2605 GGGGTGGGCAAGAACTCCAGCATGAGATCCCGCGCTGAGAGATCATCAGCGGCTC 2649  
Qy 4026 CCGAAAAAGATTCGAAAGCCCAACTTTGATGAAGCGGCGGTGGAATCGAAATCTCG 4085  
Db 2649 CCGAAAAAGATTCGAAAGCCCAACTTTGATGAAGCGGCGGTGGAATCGAAATCTCG 2705  
Qy 4086 TGATGCGAGTGGGCGTCTGTTGTCGATCAATTCGAACCCAGAGTCCGCTCAGAG 4145  
Db 2705 TGATGCGAGTGGGCGTCTGTTGTCGATCAATTCGAACCCAGAGTCCGCTCAGAG 2749  
Qy 4146 AACTCGCAAGAGCGATGAAGAGCATGCGCTGCGAATCGGAGCGGAGTATCCGTAA 4205  
Db 2749 AACTCGCAAGAGCGATGAAGAGCATGCGCTGCGAATCGGAGCGGAGTATCCGTAA 2805  
Qy 4206 AGCAGAGAGGCTCAGCCCATTCGCGCAAGCTTTCAACCAATATCAGGGTATGCC 4265  
Db 2805 AGCAGAGAGGCTCAGCCCATTCGCGCAAGCTTTCAACCAATATCAGGGTATGCC 2849

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Db 2520 AGCAGGAGGAGGCGTCAAGCCCATTCGCGCGCAAGCTTTCAGCAATATCAAGGGTAGCC 2579
Qy 4266 AAGCGTATGCTCGATAGCGGTCCGCCACACCCAGCCGCCACAGTGCATGAAATCCAGAA 4325
Db 2580 AAGCGTATGCTCGATAGCGGTCCGCCACACCCAGCCGCCACAGTGCATGAAATCCAGAA 2639
Qy 4326 AAGCGGCGATTTTCCACATGATATTTGGGAAGAGGCGATCGCATGGGTCAAGAGAGA 4385
Db 2640 AAGCGGCGATTTTCCACATGATATTTGGGAAGAGGCGATCGCATGGGTCAAGAGAGA 2699
Qy 4386 TCCTCGCGGTGAGGACATGCGCGCTTGAGCGCTGCGCAAGATTCCGCTGCGCGAGCC 4445
Db 2700 TCCTCGCGGTGAGGACATGCGCGCTTGAGCGCTGCGCAAGATTCCGCTGCGCGAGCC 2759
Qy 4446 TGATGCTTTCTGTCAGATCATCTGTATCGACAAAGACCGGCTTTCATCCGATACGTGCT 4505
Db 2760 TGATGCTTTCTGTCAGATCATCTGTATCGACAAAGACCGGCTTTCATCCGATACGTGCT 2819
Qy 4506 CGCTCGATGCGATGTTTCGCTTGATGCGAATGGGAGGTAAGCCGATCAAGCGATG 4565
Db 2820 CGCTCGATGCGATGTTTCGCTTGATGCGAATGGGAGGTAAGCCGATCAAGCGATG 2879
Qy 4566 AGCGCGCGATTTGCATCAGCCATGATGATATCTTTCTCGGCAAGAGCAAGGTGATGAC 4625
Db 2880 AGCGCGCGATTTGCATCAGCCATGATGATATCTTTCTCGGCAAGAGCAAGGTGATGAC 2939
Qy 4626 AGGAGATCTCGCCCCCGGCACTTGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTACA 4685
Db 2940 AGGAGATCTCGCCCCCGGCACTTGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTACA 2999
Qy 4686 AGCTGAGCAGCAGCTGCGCAAGAAAGCCCGTGGTGCAGCCAGCAAGTACCGCGCTGCC 4745
Db 3000 AGCTGAGCAGCAGCTGCGCAAGAAAGCCCGTGGTGCAGCCAGCAAGTACCGCGCTGCC 3059
Qy 4746 TCGTCTGCACTTCATTCAAGGAGCAGCGAAGCTCGGCTTTGACAAAGAAAGAACCGGCGC 4805
Db 3060 TCGTCTGCACTTCATTCAAGGAGCAGCGAAGCTCGGCTTTGACAAAGAAAGAACCGGCGC 3119
Qy 4806 CCGTGGCGTACAGCCCGGAAACAGGCGGCGATCAGAGAGCGATGTCGTGTCGTCGAG 4865
Db 3120 CCGTGGCGTACAGCCCGGAAACAGGCGGCGATCAGAGAGCGATGTCGTGTCGTCGAG 3179
Qy 4866 TCATAGCGAATAGCTCTCCACCCAGCGGCGGAGAACCTGCGTCAATCCATCTTGT 4925
Db 3180 TCATAGCGAATAGCTCTCCACCCAGCGGCGGAGAACCTGCGTCAATCCATCTTGT 3239
Qy 4926 TCATATGCGAAACGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4985
Db 3240 TCATATGCGAAACGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3299
Qy 4986 CAGATCTTGGCGGAGAAAGCATGATTAAGCTTTCAGAGGCTTCCCAACCTTACA 5045
Db 3300 CAGATCTTGGCGGAGAAAGCATGATTAAGCTTTCAGAGGCTTCCCAACCTTACA 3359
Qy 5046 GAGGCGCGCCAGCTGCGCAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5105
Db 3360 GAGGCGCGCCAGCTGCGCAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3419
Qy 5106 TATGCGCATGTAAGCCCATGCGAAAGCTACTGCTTCTCTT 5146
Db 3420 AACTGTGGGAAGGCGATCGGTGCGGGCTCTTCCGCTATT 3460
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RESULT 8
US-10-764-818A-14
; Sequence 14, Application US/10764818A
; Publication No. US20040204358A1
; GENERAL INFORMATION:
; APPLICANT: ADVISYS
; TITLE OF INVENTION: GROWTH HORMONE RELEASING HORMONE ("GHRH") TREATMENT DECREASES CUI
; FILE REFERENCE: 108328.00170 - AVSI-0033
; CURRENT APPLICATION NUMBER: US/10/764.818A
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; CURRENT FILING DATE: 2004-01-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 14
; LENGTH: 3534
; TYPE: DNA
; ORGANISM: artificial sequence
; OTHER INFORMATION: Sequence for the 15/27/28 GHRH plasmid.
US-10-764-818A-14

Query Match 30.4%; Score 1603.8; DB 11; Length 3534;
Best Local Similarity 82.8%; Pred. No. 0;
Matches 2022; Conservative 0; Mismatches 27; Indels 392; Gaps 1;

Qy 2706 CTAGACGTAATCATGCTCATAGCTGTTTCTGTGTGAAATTTGTATCCGCTCACAATTC 2765
Db 1412 CTTGGGTAATCATGCTCATAGCTGTTTCTGTGTGAAATTTGTATCCGCTCACAATTC 1471
Qy 2766 ACAACATACAGAGCGGAGCAATAAGGTAAAGCTGGGGTCCATAATGATGAGCTA 2825
Db 1472 ACAACATACAGAGCGGAGCAATAAGGTAAAGCTGGGGTCCATAATGATGAGCTA 1531
Qy 2826 ACTCACATTAAATTCGCTGCTCACTGCGCTTTCAGTCCGAGAACTGTCGTGCA 2885
Db 1532 ACTCACATTAAATTCGCTGCTCACTGCGCTTTCAGTCCGAGAACTGTCGTGCA 1591
Qy 2886 GCTGCATTATGATATGGCCCAAGCGCGGAGAGAGCGGTTTGCATATGGCGCTTTC 2945
Db 1592 GCTGCATTATGATATGGCCCAAGCGCGGAGAGAGCGGTTTGCATATGGCGCTTTC 1651
Qy 2946 CGCTTCCTGCTCACTGATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3005
Db 1652 CGCTTCCTGCTCACTGATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1711
Qy 3006 TCACTCAAAAGCGGTATACGCTTATCAAGAAATCAGGAGTAACGAGAAAGAAAT 3065
Db 1712 TCACTCAAAAGCGGTATACGCTTATCAAGAAATCAGGAGTAACGAGAAAGAAAT 1771
Qy 3066 GTAGAGAAAGGCGAGCAAAAGGCGAGAACCGTAAAGGCGCGTTCGCTGCTTTC 3125
Db 1772 GTAGAGAAAGGCGAGCAAAAGGCGAGAACCGTAAAGGCGCGTTCGCTGCTTTC 1831
Qy 3126 CCATAGGCTCCGCGCCCTGAGCAGAGCATCAAAATTCAGCCTCAAGTCAAGAGTGGG 3185
Db 1832 CCATAGGCTCCGCGCCCTGAGCAGAGCATCAAAATTCAGCCTCAAGTCAAGAGTGGG 1891
Qy 3186 AAACCCGAGAGCATATTAAGATACAGGCGTTTCCCTGGAAGCTCCCTGTCGCTC 3245
Db 1892 AAACCCGAGAGCATATTAAGATACAGGCGTTTCCCTGGAAGCTCCCTGTCGCTC 1951
Qy 3246 TCCTGTTCCGACCCCTGCTTACCGGATACCGTCCGCTTTCCTTCCGGAAGCGT 3305
Db 1952 TCCTGTTCCGACCCCTGCTTACCGGATACCGTCCGCTTTCCTTCCGGAAGCGT 2011
Qy 3306 GCGGCTTTCATAGTCAAGCTGATGATATCAATTCGATGATGATGATGATGATGATGAT 3365
Db 2012 GCGGCTTTCATAGTCAAGCTGATGATATCAATTCGATGATGATGATGATGATGATGAT 2071
Qy 3366 GCTGGGCTGTGTCAGAAACCCCGTTCAAGCCGAGCCGCTGCGCTTATCCGTAACCTA 3425
Db 2072 GCTGGGCTGTGTCAGAAACCCCGTTCAAGCCGAGCCGCTGCGCTTATCCGTAACCTA 2131
Qy 3426 TCCTCTTGAAGTCAACCCGTAAGAGACGATTAATGCGACCTGCGAGCGACCTGTA 3485
Db 2132 TCCTCTTGAAGTCAACCCGTAAGAGACGATTAATGCGACCTGCGAGCGACCTGTA 2191
Qy 3486 CAGATTATCAGAGCAGGATATGATGATGATGATGATGATGATGATGATGATGATGAT 3545
Db 2192 CAGATTATCAGAGCAGGATATGATGATGATGATGATGATGATGATGATGATGATGAT 2251
Qy 3546 CTAGGCTCACTAGAGAAAGATATTTGTATCTGCGCTTCTGCTGAGCGATTAACCTT 3605
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Db 1592 GCTGATTAATGAATCGGCCAACGCGGGGAGAGGGGTTTGCTATTGGCGCTTTC 1651  
Qy 2946 CGCTTCTCGCTCACTGACTGCTGCGCTCGCTGCTTTCGCTGCGGCGAGCGATACAGC 3005  
Db 1652 CGTTTCTCGCTCACTGACTGCTGCGCTCGCTGCTTTCGCTGCGGCGAGCGATACAGC 1711  
Qy 3006 TCACTCAAGGCGGATTAATGAGTTATCAGAGATTCAGGGGATTAACGAGGAAAGACAT 3065  
Db 1712 TCACCTCAAGGCGGATTAATGAGTTATCAGAGATTCAGGGGATTAACGAGGAAAGACAT 1771  
Qy 3066 GTGAGCAAAAGCGCAGCAAAAGCGCAGAACCTGTAAAGCGCGCTTGCTGCGGTTTT 3125  
Db 1772 GTGAGCAAAAGCGCAGCAAAAGCGCAGAACCTGTAAAGCGCGCTTGCTGCGGTTTT 1831  
Qy 3126 CCATAGGCTCGCCCCCTGACGAGCATCAAAAAATCGAGCTCAAGTCAAGAGTGGCG 3185  
Db 1832 CCATAGGCTCGCCCCCTGACGAGCATCAAAAAATCGAGCTCAAGTCAAGAGTGGCG 1891  
Qy 3186 AAACCCGACAGACATATAAGATACAGGCGGTTTCCCTGGAAGCTCCCTCGTGGCTC 3245  
Db 1892 AAACCCGACAGACATATAAGATACAGGCGGTTTCCCTGGAAGCTCCCTCGTGGCTC 1951  
Qy 3246 TCCTGTTCCGACCCCTGCGCTTACCGGATACCTGTCCGCTTTCCTCCCTTGGGAGCGT 3305  
Db 1952 TCCTGTTCCGACCCCTGCGCTTACCGGATACCTGTCCGCTTTCCTCCCTTGGGAGCGT 2011  
Qy 3306 GGGCCTTTCTATAGCTCAAGCTGTAGGTATCTCAAGTTCCGTTGAGTCCGTTCCCTCAA 3365  
Db 2012 GGGCCTTTCTATAGCTCAAGCTGTAGGTATCTCAAGTTCCGTTGAGTCCGTTCCCTCAA 2071  
Qy 3366 GCTGGGCTGTGACGACGACCCCGCTTCAAGCCGACCGCTGCGCTTATCCGGTAACTA 3425  
Db 2072 GCTGGGCTGTGACGACGACCCCGCTTCAAGCCGACCGCTGCGCTTATCCGGTAACTA 2131  
Qy 3426 TCGTCTTGAAGTCAACCCGGTAAGACACAGACTTATCCGCACTGCGACAGCCACTGTGTA 3485  
Db 2132 TCGTCTTGAAGTCAACCCGGTAAGACACAGACTTATCCGCACTGCGACAGCCACTGTGTA 2191  
Qy 3486 CAGAGTTAGCAGACGAGATTAAGCGGCTACAGAGTTCTTGAAGTGTGGCCCTAA 3545  
Db 2192 CAGAGTTAGCAGACGAGATTAAGCGGCTACAGAGTTCTTGAAGTGTGGCCCTAA 2251  
Qy 3546 CTACGCGTACACTAGAAAGACATATTGATCTGCGCTCTGCTGGAAGCCAGTTACCTT 3605  
Db 2252 CTACGCGTACACTAGAAAGACATATTGATCTGCGCTCTGCTGGAAGCCAGTTACCTT 2311  
Qy 3606 CGGAAAAAGAGTTGGTACTCTTGAATCCGCAAAACAACCGCTGTAGCGGTGTT 3665  
Db 2312 CGGAAAAAGAGTTGGTACTCTTGAATCCGCAAAACAACCGCTGTAGCGGTGTT 2371  
Qy 3666 TTTTGTTCGAAGCAGAGATTAAGCGGCAAAAAAGAGATCTCAAGAAAGATCCTTGAT 3725  
Db 2372 TTTTGTTCGAAGCAGAGATTAAGCGGCAAAAAAGAGATCTCAAGAAAGATCCTTGAT 2431  
Qy 3726 CTTTCTCAAGGAGTCTGACGCTCAGTGAAGAAAAACTCAGTTAAAGGATTTTGATCAT 3785  
Db 2432 CTTTCTCAAGGAGTCTGACGCTCAGTGAAGAAAAACTCAGTTAAAGGATTTTGATCAT 2449  
Qy 3786 GAGATTAATGTCGACCAAAAGCGGCAATCTGCTCCCACTCTGCAAGTTGGGGGCAATG 3845  
Db 2450 ----- 2449  
Qy 3846 GATGCGGATAGCGCGTGTGTTTCTTGATGCCAGCGATTTTGACCTCGGTAGAA 3905  
Db 2450 ----- 2449  
Qy 3906 CTCGCGAGTCTGTCAGCTTCAGGACAGACTGAACAACCTCGGAGGAGATCGAGCCC 3965  
Db 2450 ----- 2449  
Qy 3966 GGGGTGGCGAAGACTCCAGATAGATCCCGCGCTGAGAGATCATCCAGCGGCTC 4025  
Db 2450 ----- 2449

Qy 4026 CCGGAAAAAGATTCGAAAGCCCACTTTCATAGAGGGGGGCTGGAATCGAAATCTCG 4085  
Db 2450 ----- 2449  
Qy 4086 TGATGCAAGTTGGGCGTGGCTGTGTGAGTTCGAATCCCAAGATCCCGCTCAAG 4145  
Db 2450 -----CGCTCAGAG 2459  
Qy 4146 AACTGCTCAAGAAAGCGATAGAAAGCGATGCGCTGCGAATCGGAGCGCGATACCTGA 4205  
Db 2460 AACTGCTCAAGAAAGCGATAGAAAGCGATGCGCTGCGAATCGGAGCGCGATACCTGA 2519  
Qy 4206 AGCAGAGGAAGGGGTCAAGCCATTGGCCGCCAAGCTCTTCAGCAATATCAAGGATGCC 4265  
Db 2520 AGCAGAGGAAGGGGTCAAGCCATTGGCCGCCAAGCTCTTCAGCAATATCAAGGATGCC 2579  
Qy 4266 AACGCTATGCTGATAGGGTCCGCAACCCAGCGGCAACGTGATGAATCCAGAA 4325  
Db 2580 AACGCTATGCTGATAGGGTCCGCAACCCAGCGGCAACGTGATGAATCCAGAA 2639  
Qy 4326 AAGCGCATTTTTCACATGATATTCGGCAAGCAGGCAATCCGCAATGGGTCAACGAGAA 4385  
Db 2640 AAGCGCATTTTTCACATGATATTCGGCAAGCAGGCAATCCGCAATGGGTCAACGAGAA 2699  
Qy 4386 TCCTCGCGGTGGGCAATGCGCGCTTGAAGCTGGGCAACGTTGAGCTGGCGGAGCCCC 4445  
Db 2700 TCCTCGCGGTGGGCAATGCGCGCTTGAAGCTGGGCAACGTTGAGCTGGCGGAGCCCC 2759  
Qy 4446 TGATGCTCTTGTGTCAGATATCTGATGCAAGAACCGGCTTCAATCCGAGTACGTGCT 4505  
Db 2760 TGATGCTCTTGTGTCAGATATCTGATGCAAGAACCGGCTTCAATCCGAGTACGTGCT 2819  
Qy 4506 CGCTCGATGCGATTTTCCGTTGGTGTGGAAGGGCAGGTATCCGATATCCAGTATGC 4565  
Db 2820 CGCTCGATGCGATTTTCCGTTGGTGTGGAAGGGCAGGTATCCGATATCCAGTATGC 2879  
Qy 4566 AGCCGCGCATTTGATCAGCAGCATATGATGATCTTCTCGCAGAGAACAGTGAATGAC 4625  
Db 2880 AGCCGCGCATTTGATCAGCAGCATATGATGATCTTCTCGCAGAGAACAGTGAATGAC 2939  
Qy 4626 AGGAGATCTGCCCCCGCACTTCGCCAATAGACGCAAGTCCCTTCGCTTCAATGACA 4685  
Db 2940 AGGAGATCTGCCCCCGCACTTCGCCAATAGACGCAAGTCCCTTCGCTTCAATGACA 2999  
Qy 4686 ACCTCCAGCACACTGCGCAAGGAAGCCCGTGTGGCCAGCCAGATAGCCGCGTGC 4745  
Db 3000 ACCTCCAGCACACTGCGCAAGGAAGCCCGTGTGGCCAGCCAGATAGCCGCGTGC 3059  
Qy 4746 TCGTCTGCAAGTTCATTCAGGGGACCGGACAGGTGCGTCTTGACAAAAAAGAACCGGGCGC 4805  
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Qy 4806 CCTGCGCTGACAGCCGGAAACAGGGGCGCATGAGACGCCATTTGTTTGTGCCAG 4865  
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Qy 4986 CAGATCTTGTGGCGCAAGAAAGCATTCAGTTTACTTTGAGAGGCTTCCAACTTAACA 5045  
Db 3300 CAGATCTTGTGGCGCAAGAAAGCATTCAGTTTACTTTGAGAGGCTTCCAACTTAACA 3359  
Qy 5046 GAGGCGCCCCAGCTGCAATTCGAGTTGCTTGTCTGTCCATAAACCGGCCAGTACG 5105  
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Qy 5106 TATGCCATGTAAGCCACTGCAAGCTACCTGCTTCTT 5146  
Db 3420 AACTGTGGAAAGGCGATCGGTGGGCGCTTCTGCTATT 3460

RESULT 10  
US-10-764-818A-29  
; Sequence 29, Application US/10764818A  
; Publication No. US20040204358A1  
; GENERAL INFORMATION:  
; APPLICANT: ADVISYS  
; TITLE OF INVENTION: GROWTH HORMONE RELEASING HORMONE ("GHRH") TREATMENT DECREASES CUI  
; TITLE OF INVENTION: HERD ANIMALS  
; FILE REFERENCE: 108328.00170 - AVSI-0033  
; CURRENT APPLICATION NUMBER: US/10764.818A  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 29  
; LENGTH: 3534  
; TYPE: DNA  
; ORGANISM: artificial sequence  
; OTHER INFORMATION: Codon optimized plasmid for GHRH expression.  
US-10-764-818A-29

Query Match 30.4%; Score 1603.8; DB 11; Length 3534;  
Best Local Similarity 82.8%; Pred. No. 0;  
Matches 2022; Conservative 0; Mismatches 27; Indels 392; Gaps 1;

Qy 2706 CTAGACGTAATCATGTCATAGCTGTTCTGTGTAATTTGTTATCCGCTCACAAATTC 2765  
Db 1412 CTGGCGTAATCATGTCATAGCTGTTCTGTGTAATTTGTTATCCGCTCACAAATTC 1471

Qy 2766 ACACAAATACAGACCGGAGCAATTAAGTAAAGCTGGGCTCTTAATGATGAGCTA 2825  
Db 1472 ACACAAATACAGACCGGAGCAATTAAGTAAAGCTGGGCTCTTAATGATGAGCTA 1531

Qy 2826 ACTCACATTAATGCTGTGGCTCACTGCGCGCTTTCAGTCGGGAAACCTGTGATGCA 2885  
Db 1532 ACTCACATTAATGCTGTGGCTCACTGCGCGCTTTCAGTCGGGAAACCTGTGATGCA 1591

Qy 2886 GCTGCAATTAATGATTCGCGCAACCGCGGGAGAGCGGTTGGATTTGGGCGCTCTTC 2945  
Db 1592 GCTGCAATTAATGATTCGCGCAACCGCGGGAGAGCGGTTGGATTTGGGCGCTCTTC 1651

Qy 2946 CGCTTCTCGCTCACTGATCTGCTGCGCTGCTGCTGCTGCTGCGCGAGCGATACAGC 3005  
Db 1652 CGCTTCTCGCTCACTGATCTGCTGCGCTGCTGCTGCTGCTGCGCGAGCGATACAGC 1711

Qy 3006 TCACTCAAGGCGGTATAGGGTTATCAAGATTCAGAGGATTAACCGAAGAAACAT 3065  
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Qy 3066 GTGAGCAAAAGCGCAGCAAAAGCGCAAGAACCTTAAGAAAGCGCTGTCGCTTTT 3125  
Db 1772 GTGAGCAAAAGCGCAGCAAAAGCGCAAGAACCTTAAGAAAGCGCTGTCGCTTTT 1831

Qy 3126 CCAATAGCTCCGCCCTCTGACGAGCATCAAAAATCGAGCTCAAGTCAAGAGTGGCG 3185  
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Qy 3186 AAACCGCAGAGGATTAAGATACAGGCGTTCCCTCGAAGCTCCCTCGGCGCTC 3245  
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Qy 3246 TCTGTTCGACCTTCGCGCTTACCGGATACCTGTCGCGCTTTCCTCTCGGAAAGCT 3305  
Db 1952 TCTGTTCGACCTTCGCGCGCTTACCGGATACCTGTCGCGCTTTCCTCTCGGAAAGCT 2011

Qy 3306 GGGCGCTTTCATAGCTCAAGCTGTAGATCTCAAGTTGGGTAGGTGCTTCTCAA 3365  
Db 2012 GGGCGCTTTCATAGCTCAAGCTGTAGATCTCAAGTTGGGTAGGTGCTTCTCAA 2071

Qy 3366 GCTGGCTGATGTCAGCAACCCCGTTACGCCGCGATGGGCTTATCCGGTAACCTA 3425  
Db 2072 GCTGGCTGATGTCAGCAACCCCGTTACGCCGCGATGGGCTTATCCGGTAACCTA 2131

Qy 3426 TCGTCTTGAATCAACCCCGTAAAGACAGCTTATTCGCACTGCGAGCAGCACTGTAA 3485  
Db 2132 TCGTCTTGAATCAACCCCGTAAAGACAGCTTATTCGCACTGCGAGCAGCACTGTAA 2191

Qy 3486 CAGATTTAGCAGACGAGATATGAGCGGTGCTACAGAGTTCTTGAAGTGGCTTAA 3545  
Db 2192 CAGATTTAGCAGACGAGATATGAGCGGTGCTACAGAGTTCTTGAAGTGGCTTAA 2251

Qy 3546 CTAGGCTACACTAGAAAGACAGATTTGGATATGCGCTCTGCTGAAGCGAGTTACTT 3605  
Db 2252 CTAGGCTACACTAGAAAGACAGATTTGGATATGCGCTCTGCTGAAGCGAGTTACTT 2311

Qy 3606 CGAAGAAAGATTGTAGCTCTTGATCCGCAACCAACCAACCGCTGTAGCGGTGTT 3665  
Db 2312 CGAAGAAAGATTGTAGCTCTTGATCCGCAACCAACCAACCGCTGTAGCGGTGTT 2371

Qy 3666 TTTTGTTCAGACGACAGATTACGCGCAGAAAAAGATCTCAAGAGATCTTTGAT 3725  
Db 2372 TTTTGTTCAGACGACAGATTACGCGCAGAAAAAGATCTCAAGAGATCTTTGAT 2431

Qy 3726 CTTTTCACGGGGCTGACGCTCAGTGGAAACGAAACTCAGCTTAAGGATTTTGTGAT 3785  
Db 2432 CTTTTCACGGGGCTGACGCTCAGTGGAAACGAAACTCAGCTTAAGGATTTTGTGAT 2449

Qy 3786 GAGATTATCTCGACCAAGCGGCAATCGTGCTCCCACTCTGACATTGCGGGGATG 3845  
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Qy 3846 GATGCGGATAGCGCTGCTGCTGCTTCTGATGCGAGCGAATTTGACTGCGGTAGAA 3905  
Db 2450 GATGCGGATAGCGCTGCTGCTGCTTCTGATGCGAGCGAATTTGACTGCGGTAGAA 2449

Qy 3906 CTCGCGAGGTCGTCAAGCTCAGGCGAGCAGTGAACCACTCGCGAGGGAGTGAAGCC 3965  
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Db 2450 GGGGTGGCGAGAACTCAGACATGAGATCCCGCGTGAAGATCATCCAGCGCGCTC 2449

Qy 4026 CCGAAGAAAGATTCGAGAGCCCAACTTTCATAGAAAGCGCGGTGGAATCGAATCTCG 4085  
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Qy 4086 TGATGCGAGTTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4145  
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Db 2460 AACTCGTCAAGAGCGATTAAGAGCGATGCGCTGCGAATCGGAGCGCGATACGTTAA 2519

Qy 4206 AGCAGAGAGCGGTGACGCTTCTGCGCGCAAGCTTTCAAGCAATATCAAGGATAGCC 4265  
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Qy 4266 AAGGCTATGCTGATAGCGGTGCGCGCAACCGCAGCGCGCAAGCTTTCAAGCAATATCAAGGATAGCC 4325  
Db 2580 AAGGCTATGCTGATAGCGGTGCGCGCAACCGCAGCGCGCAAGCTTTCAAGCAATATCAAGGATAGCC 2639

Qy 4326 AAGCGCATTTTCAACATGATATTGCGCAACAGGCAATCGCATGCGTCAAGAGAG 4385  
Db 2640 AAGCGCATTTTCAACATGATATTGCGCAACAGGCAATCGCATGCGTCAAGAGAG 2699

Qy 4386 TCTTCGCGGTGCGGCAATGCGCGCTTGAAGCTGCGCAACAGTTGCGCTGCGCGAGCC 4445  
Db 2700 TCTTCGCGGTGCGGCAATGCGCGCTTGAAGCTGCGCAACAGTTGCGCTGCGCGAGCC 2759

QY 4446 TGA TGTCTTTCGTCAGATCATCTGTATGCAAGAACCGGCTTCATCCGATGAGTGGCT 4505  
DB 2760 TGA TGTCTTTCGTCAGATCATCTGTATGCAAGAACCGGCTTCATCCGATGAGTGGCT 2819  
QY 4506 CGCTCGATGCGATGTTTCGCTTGTGTCGAA TGGGAGGTAAGCCGATCAAGCTATGCG 4565  
DB 2820 CGCTCGATGCGATGTTTCGCTTGTGTCGAA TGGGAGGTAAGCCGATCAAGCTATGCG 2879  
QY 4566 AGCGCGCGCATTTGCATCAGCATGATGATATCTTTCTCGGAGAGCAGATGATGAC 4625  
DB 2880 AGCGCGCGCATTTGCATCAGCATGATGATATCTTTCTCGGAGAGCAGATGATGAC 2939  
QY 4626 AGGAGATCTGCCCCCGGACCTTGCCCAATAGACGCCATCCCTCCGCTTCAGTGA 4685  
DB 2940 AGGAGATCTGCCCCCGGACCTTGCCCAATAGACGCCATCCCTCCGCTTCAGTGA 2999  
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DB 3000 ACCTGAGACAGCTGCGCAAGAACCGCGTGTGCGACGACGATAGCCGCGCTGCC 3059  
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DB 3060 TCGTCTGCGAGTTGATTCAGGGGACCGGACAGGTCCGTCTTGACAAAGAACCGGGCGC 3119  
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QY 4926 TCATATGCGAAGCATCTTCATCTCTGTGATCAATCTTTGATCCCGCGCGCAT 4985  
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QY 4986 CAGATCTTGGCGGAGAAAGCATCCAGTTTACTTTGACGGGCTTCCCACTTACCA 5045  
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QY 5046 GAGGCGCGCCAGCTGCGAATTCGGTTGCTGCTGCTCAATAAACCGCCAGCTTACG 5105  
DB 3360 GAGGCGCGCCAGCTGCGAATTCGGTTGCTGCTGCTCAATAAACCGCCAGCTTACG 3419  
QY 5106 TATGCGCATGTAAGCCCATGCAAGCTACCTGCTTCTCTT 5146  
DB 3420 AACTGTTGGAGAGGCGCATGCGTGGCGCTCTTCTGCTATT 3460

## RESULT 11

US-11-186-282-22  
Sequence 22, Application US/11186282  
Publication No. US20060025368A1  
GENERAL INFORMATION:  
APPLICANT: Advia, Inc.  
TITLE OF INVENTION: Growth Hormone Releasing Hormone Enhances Vaccination Response  
FILE REFERENCE: 108328, 000265 A1SI-0042  
CURRENT APPLICATION NUMBER: US/11/186,282  
CURRENT FILING DATE: 2005-07-21  
NUMBER OF SEQ ID NOS: 41  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 22  
LENGTH: 3534  
TYPE: DNA  
ORGANISM: artificial sequence  
FEATURE:  
OTHER INFORMATION: Plasmid vector having an analog GHRH sequence.  
US-11-186-282-22

Query Match 30 4%; Score 1603.8; DB 17; Length 3534;  
Best Local Similarity 82.8%; Pred. No. 0;  
Matches 2022; Conservative 0; Mismatches 27; Indels 392; Gaps 1;

QY 2706 CTAGAGTATCATGGTGCATAGACTGTTTCTGTGTGAATTTGATTCGCTCAAGATTCC 2765  
DB 1412 CTGGCGGTAATCATAGTGCATAGCTGTTCTGTGTGAATTTGATTCGCTCAAGATTCC 1471  
QY 2766 ACACAACATACGAGCGGAGACATAAAGTGTAAAGCTGGGGTGCCTATATGATGAGCTA 2825  
DB 1472 ACACAACATACGAGCGGAGACATAAAGTGTAAAGCTGGGGTGCCTATATGATGAGCTA 1531  
QY 2826 ACTGACATTAATTGGGTGGCGCTGACCTGCGGCTTTCCAGTCGGGAAACCTGTGCTGCA 2885  
DB 1532 ACTGACATTAATTGGGTGGCGCTGACCTGCGGCTTTCCAGTCGGGAAACCTGTGCTGCA 1591  
QY 2886 GCTGATTAATGAAATCGGCAACGCGCGGAGAGAGCGGTTTGGCTATTTGGCGCTCTTC 2945  
DB 1592 GCTGATTAATGAAATCGGCAACGCGCGGAGAGAGCGGTTTGGCTATTTGGCGCTCTTC 1651  
QY 2946 CGCTTCCTGCTGACTGACTGCTGCTGCGCTCGGTGTTGGCTGCGGCGGATTCAGC 3005  
DB 1652 CGCTTCCTGCTGACTGACTGCTGCTGCGCTCGGTGTTGGCTGCGGCGGATTCAGC 1711  
QY 3006 TCACATCAAGGCGGTATACGGTTATCCACAGAAATCAGGGGATACGACGAGAAAGACAT 3065  
DB 1712 TCACATCAAGGCGGTATACGGTTATCCACAGAAATCAGGGGATACGACGAGAAAGACAT 1771  
QY 3066 GTGAGCAAAAGGCGCAGCAAAAGGCGAGAACCGTAAAGGCGCGTTGCTGGCGTTTTT 3125  
DB 1772 GTGAGCAAAAGGCGCAGCAAAAGGCGAGAACCGTAAAGGCGCGTTGCTGGCGTTTTT 1831  
QY 3126 CCATAGGCTCGGCCCCCTGAGACATTCAGAAATGAGCTCAAGTCAGAGGTGGCG 3185  
DB 1832 CCATAGGCTCGGCCCCCTGAGACATTCAGAAATGAGCTCAAGTCAGAGGTGGCG 1891  
QY 3186 AAAACCCGACAGGACTAATAAGATACAGGCGTTTCCCTGGAACCTCCCTGCGCTC 3245  
DB 1892 AAAACCCGACAGGACTAATAAGATACAGGCGTTTCCCTGGAACCTCCCTGCGCTC 1951  
QY 3246 TCCGTGTTCCGACCTGCGCTTACCGGATACCTGTCCGCTTCTTCCCTTGGGAAAGGT 3305  
DB 1952 TCCGTGTTCCGACCTGCGCTTACCGGATACCTGTCCGCTTCTTCCCTTGGGAAAGGT 2011  
QY 3306 GGGGCTTTCTCATAGTCAAGCTGATAGGATTCAGTTGAGTGTAGTGGTGGCTCCAA 3365  
DB 2012 GGGGCTTTCTCATAGTCAAGCTGATAGGATTCAGTTGAGTGTAGTGGTGGCTCCAA 2071  
QY 3366 GCTGGGCTGTGTGCAAGAACCCCGCTTCAAGCCGACGCTGCGCTTATTCGGTAACTA 3425  
DB 2072 GCTGGGCTGTGTGCAAGAACCCCGCTTCAAGCCGACGCTGCGCTTATTCGGTAACTA 2131  
QY 3426 TCGTCTTGAATCCAAACCGGTAAAGACATTTATGCACTGGACGACGCCATCGTAA 3485  
DB 2132 TCGTCTTGAATCCAAACCGGTAAAGACATTTATGCACTGGACGACGCCATCGTAA 2191  
QY 3486 CAGGATTAAGAGGAGGATGATGTAGCGGTGCTACAGAGTTCTTGAATGTGTGCTAA 3545  
DB 2192 CAGGATTAAGAGGAGGATGATGTAGCGGTGCTACAGAGTTCTTGAATGTGTGCTAA 2251  
QY 3546 CTACGGCTACATGAGAGAACATATTTGTATTTGCTGCTGCTGAGACCGATTAACCTT 3605  
DB 2252 CTACGGCTACATGAGAGAACATATTTGTATTTGCTGCTGCTGAGACCGATTAACCTT 2311  
QY 3606 CGGAAAAAGATTTGTAGCTCTTGAATCCGCAAAACAAACCGCGGTGATAGGGTGGTT 3665  
DB 2312 CGGAAAAAGATTTGTAGCTCTTGAATCCGCAAAACAAACCGCGGTGATAGGGTGGTT 2371  
QY 3666 TTTTGTTCAGACAGAGATTACGGCGAGAAAAAAGATCTCAAGAGATCTCTTGTAT 3725  
DB 2372 TTTTGTTCAGACAGAGATTACGGCGAGAAAAAAGATCTCAAGAGATCTCTTGTAT 2431  
QY 3726 CTTTTCACGGGCTGACGCTGATGGAACGAAAACTACGTTAAGGATTTTGTGTCAT 3785  
DB 2432 CTTTTCACGGGCTGACGCTGATGGAACGAAAACTACGTTAAGGATTTTGTGTCAT 2449  
QY 3786 GAGATTATGTCGACCAAGGCGCATCGTGCCTCCCACTCCTGCAAGTTCCGGGGCATG 3845

Db	2450	-----	2449
QY	3846	GATGCGGAGATAGCCGCTGCTGTTTCTGGATGCCAGCGATTGTGACTGCGGTAGAA	3905
Db	2450	-----	2449
QY	3966	CTCCGCGAGTGTGTCAACCTCAGGACAGCACTGTAACCACTCGGAGGGATCGAGCC	3965
Db	2450	-----	2449
QY	3966	GGGGTGGCGAAGAACTCAGCATGATACCCCGCTGAGAGATCATCCAGCCGCGTC	4029
Db	2450	-----	2449
QY	4026	CCGGAAAAAGATCCGAAGCCCACTTTTCATAGAGCGCGGTGGAATCGAATCTCG	4085
Db	2450	-----	2449
QY	4086	TGATGCGAGTTGGCGGTGCGTTGGTGGGTCAATTCGAACCCAGAGTCCGCTCAGAG	4145
Db	2450	-----	2459
QY	4146	AACTGTCAGAAGCGCATAGAGCGATGCGCTGCGAATCGGAGCGCGCATACCTTAA	4205
Db	2460	AACTGTCAGAAGCGCATAGAGCGATGCGCTGCGAATCGGAGCGCGCATACCTTAA	2519
QY	4206	AGCAGAGAAAGCGGTCAAGCCCATTTGCGCGCCAAAGCTTTTCAGCAATATCAAGGTAGC	4265
Db	2520	AGCAGAGAAAGCGGTCAAGCCCATTTGCGCGCCAAAGCTTTTCAGCAATATCAAGGTAGC	2579
QY	4266	AACGCTATGTCTGATAGCGGTGCGGCACACCCAGCGGCGCAAGTGAATGAATCCGAA	4325
Db	2580	AACTGATGTCTGATAGCGGTGCGGCACACCCAGCGGCGCAAGTGAATGAATCCGAA	2639
QY	4326	AAGCGGCATTTTCCACCATGATATTCGGCAAGAGCGATCGCATGCGTCAACGACGAA	4385
Db	2640	AAGCGGCATTTTCCACCATGATATTCGGCAAGAGCGATCGCATGCGTCAACGACGAA	2699
QY	4386	TCTCTGCGGTGGGCGATGCGGCGCTTGAGCTGCGGGAACAGTTGGGCTGCGCGACGCC	4445
Db	2700	TCTCTGCGGTGGGCGATGCGGCGCTTGAGCTGCGGGAACAGTTGGGCTGCGCGACGCC	2759
QY	4446	TGATGCTTTTGTGTCAGATCATTCCTGATCGAACAGCCGGCTTCATTCGAGTACGTGCT	4505
Db	2760	TGATGCTTTTGTGTCAGATCATTCCTGATCGAACAGCCGGCTTCATTCGAGTACGTGCT	2819
QY	4506	CGCTCGATGCGATGTTTGGCTTGGTGTGGAATGGGCAAGTAAAGCTACAAAGCTATGC	4565
Db	2820	CGCTCGATGCGATGTTTGGCTTGGTGTGGAATGGGCAAGTAAAGCTATCAAGGTATGC	2879
QY	4566	AGCGCGCGCATTTGATCATGAGCCATATGATATCTTTTTCGGAGAGACAGGTGATGATGAC	4625
Db	2880	AGCGCGCGCATTTGATCATGAGCCATATGATATCTTTTTCGGAGAGACAGGTGATGATGAC	2939
QY	4626	AGGAGATCTGTCGCCCGGACCTTCCGCCAATAGACAGCAGTCCCTTCCCGCTTCAGTACA	4685
Db	2940	AGGAGATCTGTCGCCCGGACCTTCCGCCAATAGACAGCAGTCCCTTCCCGCTTCAGTACA	2999
QY	4686	ACGTTCAGACAGCTGCGGCAAGAAACGCGGTGCTGTCAGCCACGATAGCCGCGCTGCC	4745
Db	3000	ACGTTCAGACAGCTGCGGCAAGAAACGCGGTGCTGTCAGCCACGATAGCCGCGCTGCC	3059
QY	4746	TGCTTCGCAATTCATTCAGGGGCAACCGGACAGTTCGCTTGAATAAAAGAACCGGGCGC	4805
Db	3060	TGCTTCGCAATTCATTCAGGGGCAACCGGACAGTTCGCTTGAATAAAAGAACCGGGCGC	3119
QY	4806	CCCTGCGGTGACAGCCGGAACACGCGCGCATCAGAGCAGCCGATTTGTCTGTGTGCCAG	4865
Db	3120	CCCTGCGGTGACAGCCGGAACACGCGCGCATCAGAGCAGCCGATTTGTCTGTGTGCCAG	3179
QY	4866	TGATAGCGGAATAGCTTCTCAACCAAGCGGCGGGAAGACTTGGTGTCAATCTTTGT	4925

[illegible]

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Db 1673 CCAATAGGCTCCGCCCCCTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGGTGGCG 1732  
Qy 3186 AAACCCGACGAGACTAATAAGATACCGAGGCTTCCCGTGAAGCTCCCTCGTGGGCTC 3245  
Db 1733 AAACCCGACGAGACTAATAAGATACCGAGGCTTCCCGTGAAGCTCCCTCGTGGGCTC 1792  
Qy 3246 TCTGTTCCGACCTGCGGCTTACCGGATACCTGTCCGCTTCTCCCTTCGGGAAAGCT 3305  
Db 1793 TCTGTTCCGACCTGCGGCTTACCGGATACCTGTCCGCTTCTCCCTTCGGGAAAGCT 1852  
Qy 3306 GGGCGTTTCTGATAGCTCAGCGCTAGTATCTCAATTCGGTGAAGTGGTGGCTTCA 3365  
Db 1853 GGGCGTTTCTGATAGCTCAGCGCTAGTATCTCAATTCGGTGAAGTGGTGGCTTCA 1912  
Qy 3366 GCTGGGCTGTGTGACGAAACCCCGCTTACGCGCCGACCGGCTGAGCTTATCCGGTAACTA 3425  
Db 1913 GCTGGGCTGTGTGACGAAACCCCGCTTACGCGCCGACCGGCTGAGCTTATCCGGTAACTA 1972  
Qy 3426 TCGTCTTGAAGTCAACCCCGGTAAACA GACTTATCGCCACTGAGCAGACCACTGTAA 3485  
Db 1973 TCGTCTTGAAGTCAACCCCGGTAAACA GACTTATCGCCACTGAGCAGACCACTGTAA 2032  
Qy 3486 CAGATTTAGCAGACCGAGGTATGTAAGCGGTACAGAGTTCTTGAAGTGGTGGCTTAA 3545  
Db 2033 CAGATTTAGCAGACCGAGGTATGTAAGCGGTACAGAGTTCTTGAAGTGGTGGCTTAA 2092  
Qy 3546 CTAAGGCTCACTAGAAAGAACATATTGATCTGCGCTCTGCTGAAGCAGTTACCTT 3605  
Db 2093 CTAAGGCTCACTAGAAAGAACATATTGATCTGCGCTCTGCTGAAGCAGTTACCTT 2152  
Qy 3606 CGGAAAAAGATTGTTAGTCTTTGATTCGGCAAAACCAACCGCTGTAGCGGTGTT 3665  
Db 2153 CGGAAAAAGATTGTTAGTCTTTGATTCGGCAAAACCAACCGCTGTAGCGGTGTT 2212  
Qy 3666 TTTTGTGTCAGAGCAGATTAACCGCGAAAAAAGATCTCAAGAGATCTTTGAT 3725  
Db 2213 TTTTGTGTCAGAGCAGATTAACCGCGAAAAAAGATCTCAAGAGATCTTTGAT 2272  
Qy 3726 CTTTCTCAAGGAGTCTGACGCTCAGTGAAGAAAACTCAGTTAAGGGATTTTGTCTAT 3785  
Db 2273 CTTTCTCAAGGAGTCTGACGCTCAGTGAAGAAAACTCAGTTAAGGGATTTTGTCTAT 2290  
Qy 3786 GAGATTATCTGACCAAAAGCGGCATCTGTCCCTCCACTCTGCAAGTTCCGGGGCAGT 3845  
Db 2291 ----- 2290  
Qy 3846 GATGCGGATAGCCGCTGTGTTTCTGATGCCAGCGATTGTGACTGCGGTAGAA 3905  
Db 2291 ----- 2290  
Qy 3906 CTCGCGAGGTCTGTCAGACTCAGGACAGCTGAACCACTCGCGAGGGATGAGAGCC 3965  
Db 2291 ----- 2290  
Qy 3966 GGGGTGGCGAAGACTCCAGATGAGATCCCGCGCTGAGAGATCATTCAGCGGCTC 4025  
Db 2291 ----- 2290  
Qy 4026 CCGAAAAAGATTCCGAAGCCCACTTTCAATAGAAAGCGCGGTGAGTGAATGAATCTCG 4085  
Db 2291 ----- 2290  
Qy 4086 TGATGCGAGTTGGCGCTGCTTGTGCTCATTTTCAACCCAGAGTCCCGCTCAGAG 4145  
Db 2291 ----- 2300  
Qy 4146 AACTGTCAAGAAAGCGATAGAAAGCGATGCGCTGCAATCGGAGCGCGATACCGTAA 4205  
Db 2301 AACTGTCAAGAAAGCGATAGAAAGCGATGCGCTGCAATCGGAGCGCGATACCGTAA 2360  
Qy 4206 AGCAGAGAAAGCGTCAAGCCCATTCGCGCGCAAGCTTTCAGCAATATCAAGGATAGCC 4265  
|||||

Db 2361 AGCAGAGAAAGCGGTCAAGCCCATTCGCGCGCAAGCTTTCAGCAATATCAAGGATAGCC 2420  
Qy 4266 AAGCTATGTCCTGTATAGCGGTTCGCCACACCAAGCCGCCACAGTCGATGAATCCGAA 4325  
Db 2421 AAGCTATGTCCTGTATAGCGGTTCGCCACACCAAGCCGCCACAGTCGATGAATCCGAA 2480  
Qy 4326 AAGCGCCATTTTCCACATATATTCCGGAAGAGAGGATGCCATGGGTTCACAGCAGA 4385  
Db 2481 AAGCGCCATTTTCCACATATATTCCGGAAGAGAGGATGCCATGGGTTCACAGCAGA 2540  
Qy 4386 TCCGTGCGGTGGGATGCGCGCTTGAAGCTTGAAGCAGTTCGCTGCGAGACCCC 4445  
Db 2541 TCCGTGCGGTGGGATGCGCGCTTGAAGCTTGAAGCAGTTCGCTGCGAGACCCC 2600  
Qy 4446 TGATGCTTTCGTCAGATCATCTGATTCAGACAGAGCCGCTTCCATCCGATAGTCT 4505  
Db 2601 TGATGCTTTCGTCAGATCATCTGATTCAGACAGAGCCGCTTCCATTCGATAGTCT 2660  
Qy 4506 CGCTGATGCGATGTTGCTTGGTGTGATGAGTGGGAGGTAGCCGATCAAGCGTATGC 4565  
Db 2661 CGCTGATGCGATGTTGCTTGGTGTGATGAGTGGGAGGTAGCCGATCAAGCGTATGC 2720  
Qy 4566 AGCCGCGCATTCATCAGACCATGATGATATCTTTCGCGAGAGCAAGGTGATGATAC 4625  
Db 2721 AGCCGCGCATTCATCAGACCATGATGATATCTTTCGCGAGAGCAAGGTGATGATAC 2780  
Qy 4626 AGGAGATCTTCCCGCGCACTTCCGCCAATAGCAGCAGTCCCTCCGCTTCAAGTGA 4685  
Db 2781 AGGAGATCTTCCCGCGCACTTCCGCCAATAGCAGCAGTCCCTCCGCTTCAAGTGA 2840  
Qy 4686 AGCTGAGCAGACGTGCGCAAGAAAGCCCGTGTGGCAGCAGATGAGCCGCTGCG 4745  
Db 2841 AGCTGAGCAGACGTGCGCAAGAAAGCCCGTGTGGCAGCAGATGAGCCGCTGCG 2900  
Qy 4746 TCGTCTGAGTTCATTTCAGGACACCGGACAGTGGTCTTGAACAAAAAGAACCGGGGCG 4805  
Db 2901 TCGTCTGAGTTCATTTCAGGACACCGGACAGTGGTCTTGAACAAAAAGAACCGGGGCG 2960  
Qy 4806 CCTGTGCTGACAGCCGGAACCGGCGGATCAGAGACCGATTGTCTGTGTGCCAG 4865  
Db 2961 CCTGTGCTGACAGCCGGAACCGGCGGATCAGAGACCGATTGTGTGTGTGCCAG 3020  
Qy 4866 TCATAGCCGAATAGCTCTTCCACCCAGAGCGCGGAGAACCTGCGTCAATCATCTTGT 4925  
Db 3021 TCATAGCCGAATAGCTCTTCCACCCAGAGCGCGGAGAACCTGCGTCAATCATCTTGT 3080  
Qy 4926 TCAATATCGAAAGCATCTCTATCTGTCTTGTATCAGATCTTGATCCCTGGCGCAT 4985  
Db 3081 TCAATATCGAAAGCATCTCTATCTGTCTTGTATCAGATCTTGATCCCTGGCGCAT 3140  
Qy 4986 CAGATCTTGGGCGGCAAGAAAGCATCCAGTTTACTTTGCAAGGCTTCCCACTTACCA 5045  
Db 3141 CAGATCTTGGGCGGCAAGAAAGCATCCAGTTTACTTTGCAAGGCTTCCCACTTACCA 3200  
Qy 5046 GAGGGCGCCCGAGCTGCAATTCGGTTGCTTGTCTGTCATPAAAACGCGCCAGTTCAG 5105  
Db 3201 GAGGGCGCCCGAGCTGCAATTCGGTTGCTTGTCTGTCATPAAAACGCGCCAGTTCAG 3260  
Qy 5106 TATCGCATGTAAAGCCCATCTGCAAGCTACCTGTCTCTT 5146  
Db 3261 AACTGTTGGAAGAGGCGATCGGTGCGGCGCTTCTGCTAAT 3301  
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RESULT 13  
US-11-194-143-27  
; Sequence 27, Application US/11194143  
; Publication No. US20060068496A1  
; GENERAL INFORMATION:  
; APPLICANT: James H. Kelly  
; TITLE OF INVENTION: Differentiation of Stem Cells  
; FILE REFERENCE: 16016.000702  
; CURRENT APPLICATION NUMBER: US/11/194,143  
; CURRENT FILING DATE: 2005-07-29

;; PRIOR APPLICATION NUMBER: 60/592,027  
;; PRIOR FILING DATE: 2004-07-29  
;; NUMBER OF SEQ ID NOS: 29  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO: 27  
;; LENGTH: 8433  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence:/note =  
US-11-194-143-27

Query Match 29.8%; Score 1572.6; DB 18; Length 8433;  
Best Local Similarity 86.3%; Pred. No. 0;  
Matches 1851; Conservative 0; Mismatches 114; Indels 180; Gaps 3;

QY 3007 CACTCAAAAGGCGGTATACGTTATCCACAGATCAGGGGATTAACGAGAAAGAAACATG 3066  
DB 5809 CACTGCAATGGCGGTAAATACGTTATCCACAGATCAGGGGATTAACGAGAAAGAAACATG 5868  
QY 3067 TGACAAAAGGCGCAAAAGGCGCAAGACCGTAAAGGCGGCTGCGCTTTTTC 3126  
DB 5869 TGACAAAAGGCGCAAAAGGCGCAAGACCGTAAAGGCGGCTGCGCTTTTTC 5928  
QY 3127 CATAGGCTCCGCCCCCTGACAGCATCACAAAATCGACGCTCAAGTCAAGGTGGCA 3186  
DB 5929 CATAGGCTCCGCCCCCTGACAGCATCACAAAATCGACGCTCAAGTCAAGGTGGCA 5988  
QY 3187 AACCCGACAGACATTAAGATACAGGCGTTTCCCTGGAAGCTCCCTGTCGCTCT 3246  
DB 5989 AACCCGACAGACATTAAGATACAGGCGTTTCCCTGGAAGCTCCCTGTCGCTCT 6048  
QY 3247 CCTGTCGACCCGCGCTTACCGGATACCTGTCGCTTTCCTCCCTGGGAAAGGCTG 3306  
DB 6049 CCTGTCGACCCGCGCTTACCGGATACCTGTCGCTTTCCTCCCTGGGAAAGGCTG 6108  
QY 3307 GCGCTTCTCATAGCTACGCTGAGGTATCTCAGTTCCGTTGAGTCTGCTCCAAAG 3366  
DB 6109 GCGCTTCTCATAGCTACGCTGAGGTATCTCAGTTCCGTTGAGTCTGCTCCAAAG 6168  
QY 3367 CTGGGCTGTGTGCAAGAACCCCGCTTCAAGCCGACCGCTGCGCTTATCCGATAT 3426  
DB 6169 CTGGGCTGTGTGCAAGAACCCCGCTTCAAGCCGACCGCTGCGCTTATCCGATAT 6228  
QY 3427 CGCTTGAAGTCCAAACCCGCTTAAAGACAGATCTATCCGCACTGGACAGCACTGGTAA 3486  
DB 6229 CGCTTGAAGTCCAAACCCGCTTAAAGACAGATCTATCCGCACTGGACAGCACTGGTAA 6288  
QY 3487 AGGATTAGCAGAGGAGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGGCTTAAC 3546  
DB 6289 AGGATTAGCAGAGGAGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGGCTTAAC 6348  
QY 3547 TACGGCTACACTAGAGAAAGATTTGTATCTGCTGCTGTAAGCACTTACCTTC 3606  
DB 6349 TACGGCTACACTAGAGAAAGATTTGTATCTGCTGCTGTAAGCACTTACCTTC 6408  
QY 3607 GGAAGAAAGATGGTGTGCTTGTATCCGGAACAAACACCGCTGGTACGGGGTTTT 3666  
DB 6409 GGAAGAAAGATGGTGTGCTTGTATCCGGAACAAACACCGCTGGTACGGGGTTTT 6468  
QY 3667 TTGTTTGCAGAGCAGATTTACCGCGAGAAAAGATCTCAAGAGATCTTTTATC 3726  
DB 6469 TTGTTTGCAGAGCAGATTTACCGCGAGAAAAGATCTCAAGAGATCTTTTATC 6528  
QY 3727 TTTTCTACGGGGCTGACGCTCAGTGGAAAGAAACTCACGTTAAGGATTTTGGTATG 3786  
DB 6529 TTTTCTACGGGGCTGACGCTCAGTGGAAAGAAACTCACGTTAAGGATTTTGGTATG 6588  
QY 3787 AGATTATCGTCACCAAGCGGCATGTGCT----- 3819  
DB 6589 AGATTATCAAAAAGATCTTCACTAGATCTTTTAAATTAAGATGTTTAAATCA 6648

QY 3820 -----CCCCACTCTCAGTTCCGG 3839  
DB 6649 ATCTAAAGTATATATGATACCTGAGGCTATAGGCAAGGCTCGCCGCCACGTTGGCT 6708  
QY 3840 GGCATGATGCGCGGATAGCCGCTGCTGTTTCTGTATGCCAGATTTGCACTGCG 3899  
DB 6709 GCGAGCCCTGGCTTCAACCGAATTGGGGGTGGGGGAAAGAAACGCG 6768  
QY 3900 G-----TAGAATCCGCGAGGTCGTCAGCCCTCAGGCAAGCTGAACCA 3945  
DB 6769 GCGTATTGGCCCCAATGAGGCTCTGTGGGGTATGCAAGATGCCAGCTGGGACCGA 6828  
QY 3946 CTCGCGAGGGGATGCA----- 3961  
DB 6829 ACCCGGGTTTATGAACAAACGACCCACACCGTGGCTTTATCTGTCTTTTATTGCC 6888  
QY 3962 -----GCCCG 3966  
DB 6889 GTCATACGCGGGTTCCTTCGGTATTTGTCTCTTCCGTGTTCACTAGCCTCCCTA 6948  
QY 3967 GGGTGGCGGAAGAACTCCACATGAGATCCCCGGCTGGAGATCATCCAGCCGCTCC 4026  
DB 6949 GGGTGGCGGAAGAACTCCACATGAGATCCCCGGCTGGAGATCATCCAGCCGCTCC 7008  
QY 4027 CGGAAAACGATTCGAAGCCCAACTTTCATAGAGGCGGCGGTGAATGAAATCTGCT 4086  
DB 7009 CGGAAAACGATTCGAAGCCCAACTTTCATAGAGGCGGCGGTGAATGAAATCTGCT 7068  
QY 4087 GATGGCAGTTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4146  
DB 7069 GATGGCAGTTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7128  
QY 4147 ACTGCTCAAGAGCGCATAGAGCGCATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4206  
DB 7129 ACTGCTCAAGAGCGCATAGAGCGCATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7188  
QY 4207 GCAAGAGAGCGGTGACCCATTCGCGCGCAAGCTTTGAGCAATATCAAGGATAGCCA 4266  
DB 7189 GCAAGAGAGCGGTGACCCATTCGCGCGCAAGCTTTGAGCAATATCAAGGATAGCCA 7248  
QY 4267 AGCTATGCTCTGATAGCGGTGCGCCACACCGCGCGCCACAGTGCATATCCAGAAA 4326  
DB 7249 AGCTATGCTCTGATAGCGGTGCGCCACACCGCGCGCCACAGTGCATATCCAGAAA 7308  
QY 4327 AGCGGCATTTTCCACATATATTGGGCAAGCAAGGATGCGCATGGGTCAACGAGAT 4386  
DB 7309 AGCGGCATTTTCCACATATATTGGGCAAGCAAGGATGCGCATGGGTCAACGAGAT 7368  
QY 4387 CTTGCGCGTGGGCAATGCGCGCTTGAAGCTTGAAGCAAGTGGGCTGGCGGAGCCCT 4446  
DB 7369 CTTGCGCGTGGGCAATGCGCGCTTGAAGCTTGAAGCAAGTGGGCTGGCGGAGCCCT 7428  
QY 4447 GATGCTTTCTGTCAGATCATCTGATTCGACAAAGACCGGCTTCACTCCAGTACGTCCT 4506  
DB 7429 GATGCTTTCTGTCAGATCATCTGATTCGACAAAGACCGGCTTCACTCCAGTACGTCCT 7488  
QY 4507 GCTCGATGCGATGTTTCTGCTGGTGTGCAATGGGCAAGGATGCGCGATCAAGCTATGCA 4566  
DB 7489 GCTCGATGCGATGTTTCTGCTGGTGTGCAATGGGCAAGGATGCGCGATCAAGCTATGCA 7548  
QY 4567 GCCCGCATTTGATCAGCATGATGATGATCTTCTCGGAGGAGCAAGGTGATGACA 4626  
DB 7549 GCCCGCATTTGATCAGCATGATGATGATCTTCTCGGAGGAGCAAGGTGATGACA 7608  
QY 4627 GGAATCTTCCGCCGCACTTCGACCAATAGCAGCCAGTCCCTTCCGCTTCACTGACAA 4686  
DB 7609 GGAATCTTCCGCCGCACTTCGACCAATAGCAGCCAGTCCCTTCCGCTTCACTGACAA 7668  
QY 4687 CGTCGACACAGCTGGCGCAAGAAAGCCGCTGCTGGCCACGACGATAGCGCGCTGCT 4746  
DB 7669 CGTCGACACAGCTGGCGCAAGAAAGCCGCTGCTGGCCACGACGATAGCGCGCTGCT 7728  
QY 4747 CGTCGTCAGTTTCACTTCAAGGCAACCGGACAGTGGCTTGAACAAAGAACCGGGGCGC 4806

Db 7729 CGTCTTGCAATTCATTCAGGCGACCGGACGATCGGTCTTGACAAAAGAACCGGCGCC 7788  
Qy 4807 CCGCGCTGACAGCCGGGACACGCGGATCAGAGAGCCGATTCGTGTGGCCAGT 4866  
Db 7789 CCGCGCTGACAGCCGGGACACGCGGATCAGAGAGCCGATTCGTGTGGCCAGT 7848  
Qy 4867 CATAGCCGAATGACCTCTCCACCCAGCGCGGAGAACTCTGCTGATTCATCTTGT 4926  
Db 7849 CATAGCCGAATGACCTCTCCACCCAGCGCGGAGAACTCTGCTGATTCATCTTGT 7908  
Qy 4927 CAATTCATGCGAAGCAATCCATCCGTCTCTGATTCAGATCTTG 4971  
Db 7909 CAATTCATGCGAAGCAATCCATCCGTCTCTGATTCAGATCTTGT 7953

## RESULT 14

US-11-005-216-4/c  
; Sequence 4, Application US/11005216  
; Publication No. US20050287633A1  
; GENERAL INFORMATION:  
; APPLICANT: McIntyre, Peter  
; APPLICANT: James, Iain Frazer  
; TITLE OF INVENTION: Human Vanilloid Receptor  
; FILE REFERENCE: 4-30875A  
; CURRENT APPLICATION NUMBER: US/11/005,216  
; PRIOR FILING DATE: 2004-12-06  
; PRIOR APPLICATION NUMBER: US/09/533,220  
; PRIOR FILING DATE: 2000-03-23  
; PRIOR APPLICATION NUMBER: UNITED KINGDOM 9907097.1  
; PRIOR FILING DATE: 1999-03-26  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Patentin Ver. 1.30  
; SEQ ID NO 4  
; LENGTH: 4886  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-005-216-4

Query Match 29.7%; Score 1570; DB 17; Length 4886;  
Best Local Similarity 86.2%; Pred. No. 0;  
Matches 1849; Conservative 0; Mismatches 115; Indels 180; Gaps 3;

Qy 3008 ACTCAAGGCGGTATAGGTTATCCACAGATCAGGGGATTAACGAGAAAGACATGT 3067  
Db 4295 AATCAATGCGGTATAGGTTATCCACAGATCAGGGGATTAACGAGAAAGACATGT 4236  
Qy 3068 GAGCAAAAGGCGCAAAAGGCGCAGAACCGTAAAGGCGCGCTTCTGGCGTTTTC 3127  
Db 4235 GAGCAAAAGGCGCAAAAGGCGCAGAACCGTAAAGGCGCGCTTCTGGCGTTTTC 4176  
Qy 3128 ATAGAGCTCCGCGCGCTGAGCAGCATCAAAAAATCGACGTCAGTCAGAGTGGCGAA 3187  
Db 4175 ATAGAGCTCCGCGCGCTGAGCAGCATCAAAAAATCGACGTCAGTCAGAGTGGCGAA 4116  
Qy 3188 ACCGCAAGAGCTATAAGATACAGAGGTTCCCGCTGAGAGTCCCTCGTGCGCTC 3247  
Db 4115 ACCGCAAGAGCTATAAGATACAGAGGTTCCCGCTGAGAGTCCCTCGTGCGCTC 4056  
Qy 3248 CTGTTCCGACCCCTGCGCTTACCGGATACGTCGCGCTTCTCCCTTCGGGAACGCTG 3307  
Db 4055 CTGTTCCGACCCCTGCGCTTACCGGATACGTCGCGCTTCTCCCTTCGGGAACGCTG 3996  
Qy 3308 CGCTTTCTCATAGCTCAGCGCTGATGTTCTCACTGGTGTAGTGGTGTCTTCAAGC 3367  
Db 3995 CGCTTTCTCATAGCTCAGCGCTGATGTTCTCACTGGTGTAGTGGTGTCTTCAAGC 3936  
Qy 3368 TGCGCTGTGTCAGAAACCCCGCTTACGCCGACCGCTGCGCTTATCCGTAATC 3427  
Db 3335 TGCGCTGTGTCAGAAACCCCGCTTACGCCGACCGCTGCGCTTATCCGTAATC 3876  
Qy 3428 GTCTTGAATCCAAACCGGTAAAGACAGATTATCGCCACTGGACAGCCACTGTGTACA 3487

Db 3875 GTCTTGAATCCAAACCGGTAAAGACAGATTATCGCCACTGGACAGCCACTGTGTACA 3816  
Qy 3488 GATTTAGCAAGCGAGATATGATGAGCGGTGCTACAGAGTTCTTTAAAGTGTGGCTAACT 3547  
Db 3815 GATTTAGCAAGCGAGATATGATGAGCGGTGCTACAGAGTTCTTTAAAGTGTGGCTAACT 3756  
Qy 3548 AGGCTACACTAGAAAGAACAGATTTGTATCTGCGCTCTGCTGAAGCGAGTTACTTCG 3607  
Db 3755 AGGCTACACTAGAAAGAACAGATTTGTATCTGCGCTCTGCTGAAGCGAGTTACTTCG 3696  
Qy 3608 GAAAAAGATTGGTACTCTTGATCCGCAACAAACACCGCTGTAGCGGTGTTTTT 3667  
Db 3695 GAAAAAGATTGGTACTCTTGATCCGCAACAAACACCGCTGTAGCGGTGTTTTT 3636  
Qy 3668 TTGTTTGCAGACAGATTAAGCCGCAAAAAAGATCTCAAGATCCTTTGATCT 3727  
Db 3635 TTGTTTGCAGACAGATTAAGCCGCAAAAAAGATCTCAAGATCCTTTGATCT 3576  
Qy 3728 TTTTCTACGGGGCTGTACGCTCAGTGAAGCAAACTCAGTTAAGGATTTTGTCAATGA 3787  
Db 3575 TTTTCTACGGGGCTGTACGCTCAGTGAAGCAAACTCAGTTAAGGATTTTGTCAATGA 3516  
Qy 3788 GATTATCGTCAACAAAGCGGCATCTGCTT----- 3819  
Db 3515 GATTATCAAAAAGATCTTCACTAGATCCTTTAAATTAAGATTTTAATCAA 3456  
Qy 3820 -----CCCCACTCCGCACTTCGCGG 3840  
Db 3455 TCTAAAGTATATATGATGATTAAGCTGAGGCTATGCGAGGGCGTCCGCCGAGCTTGGCTG 3396  
Qy 3841 GCATGATGCGCGGATGCGGCTGCTGTTCTGATGCGCAGCGAATTTGACGCGCG 3900  
Db 3395 CGAGCCCTGGGCTTCAACCGAACTTGGGGGTGGGAGAAAAAGAAAGCGCGG 3336  
Qy 3901 -----TAGAATCCGCGAGTCTGTCCAGCTTCAAGGACGACGCTGAACCAAC 3946  
Db 3335 CGTATTTGCCCAATGGGGGTCTCGGTGGGTATTCACAGAGTGCAGCGCTGGACCGAA 3276  
Qy 3947 TCGCGAGGGGATCGA----- 3961  
Db 3275 CCGCGGTTTATGAAACAAACGACCAACCGGTGCTTATCTGTCTTTTATTCGCG 3216  
Qy 3962 -----GCCCGG 3967  
Db 3215 TCATAGCGGGGTCTTCGATTTGTCTCTTCCGTGTTCAATTACCTCCCGCTAG 3156  
Qy 3968 GGTGGCGGAAGACTTCACAGATGAGTCCCGCGCTGAGATCATCCAGCGGGTCCC 4027  
Db 3155 GGTGGCGGAAGACTTCACAGATGAGTCCCGCGCTGAGATCATCCAGCGGGTCCC 3096  
Qy 4028 GGAAGAGATTCGGAAGCCCACTTTCATAGAGGCGCGGTGGAATCGAATCTCTG 4087  
Db 3095 GGAAGAGATTCGGAAGCCCACTTTCATAGAGGCGCGGTGGAATCGAATCTCTG 3036  
Qy 4088 ATGCGAGTTGGCGTCTGCTGCTGATTTGAACTCCAGAGTCCGCTGAGAGAA 4147  
Db 3035 ATGCGAGTTGGCGTCTGCTGCTGATTTGAACTCCAGAGTCCGCTGAGAGAA 2976  
Qy 4148 CTGCTCAAGAGGCTATAGAGGCTATGCGCTGCGCAATGGGAGCGGCGATCCGTAAG 4207  
Db 2975 CTGCTCAAGAGGCTATAGAGGCTATGCGCTGCGCAATGGGAGCGGCGATCCGTAAG 2916  
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Qy 4268 CGCTATGCTCTGATGAGCGGTCCGCAACCCAGCGGCAAGTGTATGATTCAGAAAA 4327  
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Qy 4328 GCGGCAATTTTCAACATATATTCGGCAAGAGGATGCGCAATGGGTCAAGCAGATC 4387  
Db 2795 GCGGCAATTTTCAACATATATTCGGCAAGAGGATGCGCAATGGGTCAAGCAGATC 2736







Db 3127 CGTTATGAACAAACGACCCAGCCGTTTATTCTGTCTTTTATTGCCGTATA 3068  
QY 3962 -----GCCGGGGTGG 3972  
Db 3067 GCGCGGGTTCCTCCGGTATGTCTCCTCCGTTTCACTAGCTCCCTTAGGGTGG 3008  
QY 3973 GCGAAGAACTCCAGCATGATGCCGGGCTGAGGATCATCCAGCGGGCTCCGGAAA 4032  
Db 3007 GCGAAGAACTCCAGCATGATGCCGGGCTGAGGATCATCCAGCGGGCTCCGGAAA 2948  
QY 4033 ACGATTCCGAAGCCCAACTTTCAAGAGCGCGGTGGAATGAAATCTGTGATGC 4092  
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QY 4153 CAAGAAAGCGATGAGAGCGGCTGCGAATCGGAGCGGCGATACCGTAAAGCAGA 4212  
Db 2827 CAAGAAAGCGATGAGAGCGGCTGCGAATCGGAGCGGCGATACCGTAAAGCAGA 2768  
QY 4213 GGAAGCGGTCAAGCCATTGCGCGCAAGCTTTCAAGCAATATCACGGGTAGCCACGCTA 4272  
Db 2767 GGAAGCGGTCAAGCCATTGCGCGCAAGCTTTCAAGCAATATCACGGGTAGCCACGCTA 2708  
QY 4273 TGTCTGATGAGCGGTCCGCCACACCCAGCGGCCACAGTGAATCCAGAAAAGCGGC 4332  
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Db 2107 CGAATAGCTCTCTCAACCGGCGGAGAACCTGCGCAATCCATCTTGTTCATCA 2048  
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